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AB010708 Gentlana
E12757 Senecio cru
E12754 Gentlanatri
AB026494 Gentlana
E12756 Perilla oci
AB029340 Perilla f
AC003027 Arabidops
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E12757
E12754
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                                                                November 5, 2001, 13:50:30 ; Search time 8904.87 Seconds (without alignments) 2958.109 Million cell updates/sec
                                                                                                             2688314
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                           OM nucleic - nucleic search, using sw model
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unidentified unclassified.

ORGANISM

REFERENCE AUTHORS

KEYWORDS SOURCE

DEFINITION

ACCESSION VERSION

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TITLE JOURNAL

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SOURCE	REFERENCE AUTHORS	TITLE	REFERENCE AUTHORS	TITLE	JOURNAL MEDLINE FEATURES SOUICE	;	SOS			polyA_s	BASE COUNT	Query Ma Best Loc Matches	1 1	Qy 61 CT	Oy 121 AC 11 Db 121 AC	Qy 181 TG
840	006	096	1020	1080	1140	1200	1260	1320	1380	1440	1500	1560	1620	1680		
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AB010708 1679 bp mRNA PLN 20-FEB-1999 Gentiana triflora mRNA for Anthocyanin 5-aromatic acyltransferase,

DEFINITION

ACCESSION VERSION KEYWORDS

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RESULT AB010708 LOCUS complete cds.
AB010708
AB010708.1 GI:4185598
Anthocyanin 5-aromatic acyltransferase.

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SKRFLGITGSPKFDSYGVDFGKGRPAKFDITSVDYAELIYVIOSRDFFEKGVEIGVSLP
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                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentlanales; Gentlanaceae; Gentlana. 1 (bases 1 to 1679)
Fujiwara, H., Tanaka, Y. and Kusumi, T.
                                                                                                                                                                                                                                                                                                                                2 (sites)
Pujiwara, H., Tanaka, Y., Yonekura-Sakakibara, K.,
Fukuchi-Mizutani, M., Nakao, M., Fukui, Y., Yamaguchi, M., Ashikari, T.
and Kusumi, T.
                                                                                                                                                                                           Submitted (22-7AN-1998) to the DDBJ/EMBL/GenBank databases. Hiroyuki Fujiwara, Suntory LTD., Inst. of Fundamental Research; 1-1-1, Wakayamadai, Shamamoto-cho, Osaka 618-0024, Japan (E-mail:Hiroyuki_Fujiwara@suntory.co.jp, Tel:+81-75-962-8807, Fax:+81-75-962-8262)
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Gentiana triflora petal cDNA to mRNA, clone:pGAT4. Gentiana triflora
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/db_xref="taxon:55190"
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100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PI FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKA C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10,C12R1:865),
CC (C12N9/10,C12R1:19);
CC strandedness: Double;
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                    ACCACCACGAGGTTCAATCACTAGAAGGTTGTACTTCATAAATTCCAGAGGTCGAATATA
                                                                                         TGAAGGTTCTTGAAAAATGCCAAGTTACACCACCATCTGACACAACAGATGTCGAGTTAT
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ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI,
MASAHIRO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fukui, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVITY
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Senecio cruentus mRNA for acyltransferase,,partial cds.
E12757
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M.,
Yonekura,K., Mizutani,M. and Kusumi,T. .
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER
PATENT: JP 1997070290-A 5 18-MAR-1997;
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/tissue_type='petal'
/clone='pCAT48'
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/organism="unidentified"
/db_xref="taxon:32644"
1 293 c 296 g 477
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17-FEB-1995 JP 95P 671
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JP 1997070290-A/5
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11; Conservative
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Matches 721;
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CGCTACCGGTAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTC 144
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VERSION
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JOURNAL
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SOURCE
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                                                                                                                                CGGGTATATCACTAGGAATGACGATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCA
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CGTTATCTCTTACTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTT
                        TGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTAATCTTA
                                   AGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGC
                                                                                                                                                               ACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAAGGTCATC
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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AGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACCT 1275
                                                                                                                                             1336 AGATTGGAGTATCATTGCCTAAGATTCATATGGATGCATTTGCAAAAATCTTTGAAGAAG 1395
                                                                                                                                                              57 TCAAAGTTCTTGAGAAATGCCGTGTTGCCGCCCCCCCCGGAC---GCCGTCGCCCGGGTTA 113
                                                                                                                                                                                                                                                                                                                                        E12754 1622 bp DNA PAT 24-JUN-1998 Gentianatriflora mRNA for acyltransferase, complete cds. E12754 1 GI:3251586 JP 1997070290-A/2. unidentified.
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PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASSHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
MASAHIRO,
                                                                                         CTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCAGGGATTTTGAAAAGGTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l (bases I to 1622)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE COLING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
SUNTORY LTD
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    /organism='Gentiana triflora'

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Pred. No. 1e-37;
0; Mismatches 618; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type='petal'
/clone='pGAT106'
35. .1474
/product='acyltransferase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
1 345 c 322 g 47
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strandedness: Double;
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JP 1997070290-A/2
18-MAR-1997
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11.1%;
Best Local Similarity 52.2%;
Matches 728; Conservative (
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                                           TGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCTAATCTTA
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TGICIGRNLHQVLGARSFLHFNKLWYLNDSRNGSNGSKFLFLESLEWYDRSVVODPFH
IRRIYNERKLLKSQGTPTVLNPAISKDEVRATFILHPIDIMKLKKFISSRNRNLTGS
SYNLGFFTYTYSALLWYCSKSLDYVREKVEBERHAANLGAFINCROFFAPP
FGNCIYPCANGSTHEDLYGNGGLSVAAATAIGDAIHKRLHDYSGILAGDWISPPRSTSA
APRSTLIYVVGSAQRNVHDFDAADFGKLEKHESVSTNPSAILLISRSRRFKGALEL
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                                          AAAAGCATGAATCTGTTTCAACTACCTTCGGCAACACTAATTTTGATCTCTCGGTCCA 1358
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Fujiwara,H., Fukui,Y., Toshihiko,A., Yamaguchi,M. and Kusumi,T.
Molecular cloning and blochemical characteization of
hydroxycinnmamoyl-Coa.anthocyanin
3-0-glucoside-6-0-hydroxycinnamoyltransferase from Perilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)

(Loases 1 to 162)

Tanaka,Y. and Yonekura-Sakakibara,K.
Direct Submission
Submitted (21-APR-1999) to the DDBJ/EMBL/GenBank databases.
Yoshikazu Tanaka, Suntory Ltd., Institute for Fundamental R Wakayama-dai 1-1., Shimamoto, Osaka 618-8503, Japan (E-mail:Yoshikazu_Tanaka&Suntory.co.jp, Tel:81-75-962-8807,
                                                                                                                                   CAAAATTTGACA - - - TTACCTCTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCA
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/protein_id="BAA93452.1"
/db_xref="GI:7415597"
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/db_xref="taxon:55190"
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strandedness: Double;
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JP 1997070290·A/4
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          Length 1622;
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16-37;
                             0; Mismatches 618;
         11.1%; Score 189.2;
llarity 52.2%; Pred. No. 1e-3
Conservative 0; Mismatches
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Perilla ocimoides mRNA for acyltransferase, partial cds.
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PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
PI FUKUI YUKO. VANDENTI.
                    1179 ATTGGATATCGCCCCCCGATCAACATCTGCGGCACCAAGGTCGACGCTCATTTATGTCG
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutáni,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 4 18-MAR-1997;
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/organism='Perilla
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/organism="unidentified"

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                       Gaps
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                                                                                        TCCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCT
                                                                                                                                   AATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTG
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                       48;
 Length 1479;
                      0; Mismatches 668; Indels
DB 10;
           Pred. No. 2.2e-33;
Score 172.2;
 10.1%;
          49.58;
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/translation="VIETCRVGPPPDSVAEQSVPLTFFDMTWLHFHPMLQLLFYEFPC
SQPGPSESTYVPKLKQSLSKTLLHFFPLSCNLITPSSPERMPEPRILSCDSVSFFTTAES
SDPFDDLVGNRPESPYRLYNFPVKLPPTVESDRKLFQVFAVQVTLFPGRGVGIGIAT
HHTVSDAPSFLAFITAMSSMSKHIENEDBEBEFKSLPVFDRSVIKYPTKFDSIYWRNA
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TITKSFTRADEODUBDAFFLIPVDLRPRPENDFYDFONTSFONCLSYALPRWRRELVGEKG
VFLAARDIAAEIKKRINDKRILETVERWSPEIRKALOKSYFEVASSKLDLYGADFGW
GKARKQEILSIDGEKYAMTLCKARDFEGGLEVCLSLPKDKMDAFAAYFSLGING"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB029340 1476 bp mRNA PLN 04-APR-2000
Perilla frutescens mRNA for anthocyanin acyltransferase, partial
                                                                                                                                                               AAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACC 1274
                                                                                                                                                                                                     TCGATTGATGGGGAGAAATATGCAATGACRCTTTGTAAAGCCAGGGATTTCGAAGGAGGA 1265
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TGGTTATCGGAATCTAATGGAATCCCTTCAAAAAGATTTCTCGGGATTACCGGATCGCCT
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                                                                           TGGTCGCCGGAGATTCGTAAAGCGTTGCAGAAATCATATTTTCGGTGGCAGGATCGAGC
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2 (bases 1 to 1476)
Sakakibara, K.Y. and Tanaka, Y.
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Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla
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/protein_id="BAA93475.1"
/db_xref="GI:7415646"
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Spermatophyta; Magnoliophyta; eudicotyledons;
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    1476
    /organism="Perilla frutescens"
/db_xref="taxon:48386"

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Perilla frutescens leaf cDNA to
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Burasicales; Brassicaceae; Arabidopsis.

1 (bases i to 119914)
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1 Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

Unpublished
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Direct Submission
GTGGAGATTGGAGTATCATTGCTAAGATTCATATGGATGCATTTGCAAAAATCTTTGAA 1391
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                                                         GGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACT
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Stanford University, 855 California Avenue, Palo Alto,
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                                                                         Length 1476
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jóln(20752. .20994,21362. .21497,21596. .21740,21825. .21994,
22102. .22178,22542. .22758,22920. .23064,23343. .23442,
23599. .23693,24021. .24072,24227. .24298,24441. .24647)
/gene="F2IM11.5"
/translation="MDRTMFLSLTIASLLVGVVSAGDWNILNQLRGLGSSSSQNGIVS
KGIRTDLKGVCESWRINVEVHNIRKEDVVPGGCVSHIKDVFWTSSQYKDDVARTVDBVI
LHFGSMCCSKSKCDGMDAWIFDIDDTLLSTIPPHKRNGFFGGERLNSTRFEDWIQKKK
APAVPHKKLYHDIFREKGIKIFLISSRKEYLERSATVDNLIQAGYYGNSNLMLNGLEDQ
OKEVKQYKSEKRKWLMSLGYRVWGVMGDQWSSFAGCPLPRRTFKLNSIYYVA"
complement(join(14004. 14312, 14565. 14641, 14787. 15831, 15906. 16006, 16327. 16362))
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KWLDQHIAPYFAVGAPLLGSYBAIKSTLSGYPTGLEVSEGTARLLSNSFASSLWIMPF
SKNCKGDNTFWTHFSGGAARKDRRVYHCDEEFYQSYSGWPTNINIEIPSTSARELA
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BRPPIKNVFCIYGAHLKTEVGYYFAPSGKPYPDNWIITDIIYETEGSLVSRSGTVVDG
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LAVDASLSYWLSTSEGSECNSASWTLTPEKLKSTGCYSKPLRINHDDRPVLCALTL
EDIKQFSATSTPRKSPEKSPDETPIIGTVGCYWGNRSKAIDCGSASSFKGIPNTSSKY
REDKGYWHGTPFERALEKALNNIDK"
COMPLEMENT (16835. . . 20238)
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PQYYEGDIYKNRIKABELARMAKIKCYKCSLKGAALGGFVKSCRRSYHVPCAREISRCR
WDYDDFLLLCPAKISYNKPURIKSGHRVSRABELPKINPAELGSLEGOPPAFTKELVLCG
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ILNAAMMKSALKASQPVDESPFENQIDTOGCOGOPOKTARLRABENKPKLEGGIKFYFF
GDFYKGYKEDLQULYKVAGGTILNTEDELGAESSNNVNDQRSSSIVVXNIDPHGGAL
GEEVTIIWQRANDAEALASQTGSRLVGHTWVLESIAGYKLHPVIG"
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FESEYDAAMHTPESYTEQSAKRWPDTTTASEQFSMAAKRIGGDSFIQESSPUPKTQDP
TLLRAMESLRSDDPTDVVKAQNHQMYFSFWJTYSFVLCLRSNNLRCVVIFCYQQLPK
SHTEQDSKRKRDITASDAMENHLKVPKRENNLMQKSADIDCNGKCSANSDDQLSEKIS
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IIDGFASTQLRAWSILDCPYTPLDFNPLDLVWLDTTKLLSAVNCWFKCMVLDPYNQTD
HPECKSRPDSGLSAITELDPGYITGPLSTVWKEWLKWCVEFGIEANAIVAVPYDWRLS
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ICDEAEEKCSPSTISRKRVTFDSKVKTYEHVVSEESVELSEEKNEEVESEKRSLKSSK
TDDQIIEVASNSSGSYPENHRYKNCRESDDDIEEDEFDCSDSDLDEDEEYYSDVGFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(16835. 17185,17274. 17392,17491. 17656, 17795. 17885,17982. 18079,18175. 18361,18504. 18604, 18705. 19049,19134. 19349,19439. 19791,19862. 19967, 20188. .20238))
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HEHGSDIIANMTKAPRVKYITFYEDSESIPGKRTAVWELDKSGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(14567. .14641,14787. .15831,15906. .16006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16327. .16362))
/gene="F21M11.3"
/notc="Unknown protein; Location of ESTs 40C3TT,
gb|AA728590 and40C3T7, gb|T04573"
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                                                                                                                                                                                                                                                                                                                                                                                complement(14004. .16362)
/gene="F21M11.3"
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/db_xref="GI:4204287"
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/db_xref="G1:4204286"
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/gene="F21M11.5"
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/gene="F21M11.6"
27777. .28734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AC002560).
e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described as
'putative', 'like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'.
Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
http://gnomic.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev
& A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and
NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
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DDAYKVLLDAFTEDEADAQSTEKNKKEEERKKREKERKSRKSPASTRGRRKAFEPELVQDEE
DDAWDEDEFFEKRRERSRRGRASSSSSSSSSNNEDLKTQPEEEDEDGGVTELPPLKRY
VRRNGERGLAMTVYNNASPSSSSRLSMEPEEVPPMVLLPAHPMETKVSEASALVILND
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SEHKVAAAASVELASSTSGEAKICLSFAPATGETTNLHLPSMEDLRRAMEEKCLKSYKI
VHPEFSVLGFMKDMCSCYIDLAKNSTSQLLETETVCDMSKAGDESGAVGISMPLVVVP
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SESFBORGSCSTSCIEDCLASEMSCWONGIGVDWFGAYTUDGLLKEEFLEARISFARDQ
RKOVLRFCEECPLEARKVEILEPOKGHLKRGAIKEOWFKCGCTKRCGNRYOGRMHY
KLOVFFTPNGKGWGLRFLEKLPKGAFICEYIGEILJIPELYORSFEDKPTLPVILDAH
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SDEBAMEELAMDYGIDFNDNDSLMRPPCLCGSRFCRRKKRSTKTMQILNKA"
join(13033. 11488,13717. 13926,14139. 14514)
/gene="F21M11.2"
join(1303. 14514
/gene="F21M11.2"
join(13061. 13488,13717. 13926,14139. 14316)
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1. 9262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone
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                   Buehler, E., Dunn, P.,
                                                                                                                                                                                                                                               Submitted (30-JAN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
         Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P. Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Lucs,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                          of
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                                                                                                                                                                                                                                                                                                                                                                                On Dec 30, 1998 this sequence version replaced gi:2734094.
Bases 1-926 of clone F2LM1 overlap with bases 68998-78259 of TARUY BAC clone F2DD22 (ACO02411) and bases 119525-119914 of F2LM11 overlap with bases 1-389 of 'TAMU' BAC clone F2LDS
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110C2T7 , gb[f42036, and 110C2XP, gb[AI100245"
/codon_start=1
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/db_xref="G1:4204284"
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/db_xref="G1:4204285"
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/chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .119914
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/gene="F21M11.1"
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Arabidopsis thallana
Bukaryotats, tracheophyta; Spermatophyta;
Bukaryotat; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryotat; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brassicales; Brassicaceae; Arabidopsis.
Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 101176)
Shinn,P., Altafi,H., Bel,Q., Chin,C., Chiou,J., Chol,E., Conn,L.,
Shinn,P., Altafi,H., Bel,Q., Chin,C., Chiou,J., Chol,E., Conn,L.,
Lee,J., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N.,
Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A.,
Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Federspiel,N.A.,
Theologis,A. and Ecker,J.R.
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Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome
I, complete sequence.
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Submitted (25-SEP-1997) Arabidopsis thallana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
3 (bases 1 to 101176)
1213 CTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTA 1272
                                                                                                                                                                                                                                                                                                                                                                                                      47073 GGGGACAAGGACTACATAATGGGTCATGTCCCATTATCCAACTCAATTGCAGGGGGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46836 ACGAGGAAGAAGGATGAAGGATTTCACTTGATGATCAATGTGGATTGCAGGAATCGCC
                                                                                                                                                          TTGGAGAAGCCATTGAAAAGAGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAA
                                                                                                                                                                                                                                                                                                                                      47016 TCACAGCGAGAATCAAAGATATGTTATCAAGCG---ATCTGTTGAAGACAGCACCAAGAT
                                                                                                                                                                                                                                                                                                                                                                                CTTGGTTATCGGAATCTAATG3AATCCCTTCAAAAAGATTTCTCGGGATTACCGGATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1273 CCTCTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCAGGGATTTTGAAAAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47193 TGCACATAGAAACAGGTGGTTCTATCGCATTCTCAGAGTCCAGAGACGGCAGCAATGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAGATTGGAGTATCATTGCCTAAGATTCATATGGATGCATTTGCAAAAATCTTTGAAG
                                                           CATCGAACGACGAAAATGAGCCCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGACTTC
                                                                                                                                                                                                                     CAAAAGCAACACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTA
                                                                                                                                       T-----GACGCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCGTCATGCGTTG
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Direct Submission
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SOURCE
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                                                                                                               /protein_id="Aad10670.1"
/db_xref="G1:4204289"
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                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                      /gene="F21M11.7"
complement(join(29264. .31015,31312. .31414,31484. .31587,
31782. .32033))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46187
                                                                                                                                                                                                                                                                                                                                                                                                                                     CICITCCICICACCTICITCGATGCCCCCTGGCTCTCTCCCCACTCGCCGATTCTCTCT 46067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGAATTCAGATGCGACCAATAATGGCTATGCAAGTCACCATCTTCCCTGGAGCTGGAA 46421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46422 TCTGTATAGGCAACTCAGCTACACATGTTGTAGCAGATGGAGTCACCTTCAGTCATTTCA 46481
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACATITGGAGGGGTTTTGGAGGCCAAAACTCTGCAAAACACAGGTTCACATGTTACGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           742 TCAACAAGGTACGAGCTACATATGTCCTCCCTTGCTGAAATCCAGAAGCTAAAGAACA
                                                         ESTS 203124T7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACATTCCCTCTCCATCACTCTCCCAACATTCTTCCCTTACGCCGGTAAACTGATTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 TAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46482 TGAAGTATTGGATGTCATTGACCAAATCCAGCGGTAAAGATCCCGCCACGGTTCTTCTAC
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                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                  Length 119914;
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                         Location of gb|AA605510"
                                                                                                                                                                                                                                                                                                                  6.7%; Score 114; DB 12;
llarity 46.2%; Pred. No. 2.8e-18;
Conservative 0; Mismatches 685;
                                                                                                                                                                                                                   complement(29264. .32033)
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gb|H76794 and 203124XP,
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                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 612;
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join(11965. .12033,12173. .12303,12448. .12519,12596. .12685,
12786. 12915,12985. .13041)
//note="similar to ATHP1 dbj|BAA37110.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              VTEFTCGGFSLGIRLCHCICDGFGAMQFLGSWAATAKTGKLIADPEPVWDRETFKPRN
PPMVKYPHHEYLPIEERSNLTNSLWDTKPLQKCYRISKEFQCRVKSIAQGEDPTLVCS
TFDAMAAHIWRSWVKALDVKPLDYNLRLTFSVNVRTRLETLKLRKGFYGNVVCLACAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /traislation="MOHDSFCYLIVLRCALRCGITALMQICALQKKERRSKMESSDRS
SQARAFDERKTGVKGIVASGIKEIPAMFHTPPDTLTSLKQTAPPSQQLTIPYVDLKGG
SMDLISRRSVVEKIGDAAERWGFFQVVNHGISVEVBERMEGIRRFHEQDPEVKRFY
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MTLGEFLFELLSEALGLNPNHLKDMGCAKSHIMFGQYYPPCPQPDLTLGISKHTDFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITILLQDNIGGLQVIHDQCWVDVSPVPGALVINIGDLLQLISNDKFISAEHRVIANGS
SERTSMPCFCYSTFWRENPREXTEQTERLLESQDARKYRDLITTESRYFERSOTFRITE
SEPALEMPCFYSTFWKSPPPRHITITTVDIKGNASKYREKIGEAAEKWGLEHLVNHGIP
VEVLERMIQGIRGFHEQGEPEAKKRFYSRDHTRDVLYFSNHDLQNSEAASWRDTLGCYT
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VORGHYPROPODLITGINKHDISFCHZLLDNVGGLQVFREDYWIDYPPVGALAVIN
IGDFLQVXKI MLLLEYSCFISCHIMGLILLFYCVQLITNDKFISAEHVIANGSSEPRT
SVAIVFSTFWRAYSRVYGPIKDLLSAENPAKYRDCTLTEFSTIFSSKTLDAPKLHHFR
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vaevvslffddcsklintmsislerpdnvdfkqvdsgvydkgsssslcfvlsvgarr
vknvcisfkeccdvqnregyssnshtncdndiwhrclrclqqvdyfykmlktklqdlf
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EVFFGEEQGVLMVSANSSMDLADLGDLTVPNPAMLPLIFRNPGEEAYKILEMPLLIAQ
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SKFFESWDFTSDPCGFAGVYCNGDKVISLNLGDPRAGSPGLSGRIDPAIGKLSALTEL
SIVPGRIMGALPATISQLKDLRFLAISRNFISGEIPASLGEVRGLRTLDLSYNQLTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSVESLINDSLSKTTRLVQDARLRVSEDYLRSMVDYVDVKRPKRLEFGGKLTITQWTR
FEMYETADFGWGKPVYAGPIDLRPTPQVCVLLPQGGVESGNDQSMVVCLCLPPTAVHT
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/note="similar to protein kinase pir||A57676; similar to
ESTS gb|A1993651.1, dbj|AV538995.1, dbj|AV522524.1, and
dbj|AV538995.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(6700. .7357,7482. .7884,8620. .8839,
8920. .9241,9758. .10380))
//note="unknown protein; similar to ESTs gb|T04168.1,
9B|T21964. .1, and gb|AW004462.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="unknown protein; similar to EST emb|230724.1"
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          /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                         /evidence=not_experimental
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/product="F21B7.5"
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/db_xref="GI:9280641"
                                                                                                                                                                                                   /protein_id="AAF86541.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:9280671"
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Makharsky, Kim,C., Altafi,H., Bei,B., Chin,C., Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bei,B., Chin,C., How,Ing,B., Koo,T., Lan,S., Liu,S., Mukharsky,N., Rouen,M., Palm,C., Liu,J., Liu,A., Liu,J., Liu,S., Mukharsky,N., Rouen,M., Palm,C., Liu,J., Liu,A., Liu,J., Liu,S., Mukharsky,N., Rouen,M., Palm,C., Dama,D., Sakano,H., Vu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J.

Direct Submission

Submitted (19-JUL-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                         Direct Submission

Loungted (26-JAN-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (Dases 1 to 101178)

E (bases 1 to 101178)

Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Li, J., Liu, J., Liu, J., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submission

Loungted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
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DLQLNSRTNALEHILVYTPSGHVVQHELLPSVCTESPENGLRVQKTSHVQVQEDDLRV
KVEPIQWWDVCRRSDWLETEERLPKSITEKQYDLETVSNHLTSHEDACLSLDMNSHFS
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INCHSKPGSIESAESSEEGSTKOMENLHDSDHMSNSIKSSLPLYPTVNGIYKEIEKNN
ANGWMEKPVTAKLSTLKETRITNGFTTPPILLTDSVNEOMLSTGKPPMGFGFALHEEHC
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                              Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

(bases 1 to 101176)
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3117. .3274,3483. .3610,3725. .4134,4313. .4435)
/note="unknown protein: similar to ESTS dbj|AV529515.1,
dbj|AV529266.1, dbj|AV554950.1, dbj|AV523761.1,
dbj|AV522761.1, dbj|AN5996703.1, and dbj|AV546743.1"
Submitted (13-NOV-1997) Arabidopsis thaliana Genome Center,

    .101176
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"

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/evidence=not_experimental
/product="F21B7.1"
/protein_id="AFRB6508.1"
/db_xref="G1:9280639"
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                                                                                                                                                                                                                                                     Direct Submission
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PQNIVCGHTLTAVFVNNSHOLILFGGSTTAVANHNSSLPEISLDGVTRSVHSFDVLTR
KWTRLNPIGDVPSPRACHAAALYGTLILIGGGIGPSGPSDGDVWLDMTNNKWIKFLV
GGETPSPRYGHVMDIAMLVIFSGONELLDDTWALDTRGPFSWDRLNPSGNQPS
GRMYASGSSREDGIFLLCGGIDHSGYTLGDTYGLKMDSDNVWTPVPRAPAPSPRYQHTA
VFGGSKLHVIGGILNRARLIDGEAVVADTNOPETSASGANRQNQYQLMRRCHHAAASF
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ISPSIGSLPELSNLILCHNHLTGSIPPFLSQTLTRIDLKRNSLTGSISPASLPPSLQY
LSLAWNQLTGSVYHVLLRLNQLNY LDLSLNRFTGTIPARVFAFPITNLQLQRNFFFGL
                                                                    IQPANQVTISTVDLSYNRFSGGISPLLSSVENLYLNSNRFTGEVPASFVERLLSANIQ
                                                                                          TLYLQHNFLTGIQISPAABIPVSSSLCLQYNCMVPPLQTPCPLKAGPQKTRPTTQCTE
WRG"
                                                                                                                                                     complement(join(18462..18515,18612..18742,18840..18975,19064..19139,19214..19410,19497..15955,19668..19752,19865..20103,20179..20159.20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..201799..20179..20179..20179..20179..20179..20179..20179..20179..2017
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ilarity 44.9%; Pred. No. 4.6e-17;
Conservative 0; Mismatches 708;
                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/product="F21B7.7"
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AHARONI ASAPH (IL) ; VERHOEVEN HARRIE ADRIANUS (NL) ; LUECKER JOC (NL) ; CPRO DLO (NL) ; CONNELL ANN PATRICIA O (NL) ; TUNEN ARJEN
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Aharoni, A., Verhoeven, H.A., Luecker, J., O'Connell, A.P. and
                                                                                                       TTACAGAGC-----AGTCTGAGAATCAATCTCCTGTTTCTACCTTCGTGGTGACTCTAG
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PTPODAUGSTSTAVSHAILDGKTSTLELKSGNAYCKOLDLCHHPCLSPELTPLLDRY
VIKDPTGQDMLQLNKWVGSDNSDPQKIRSLKVLPFLDSESLNKLVRATFELTREDIT
KLRHKVNHQLSKSSKSKQVRLSTFVLTLAYVFVCMKAKLKAKAKTEREAAAGNDEIKN
IVGFTADYRSRLDPIPLNFGCNGRHCETAKASDFVQENGVATSEAAAGNDEIKN
IVGFTADYRSRLDPIPLNFGCNGRHCETAKASDFVQENGVAFWLSDWYKGI
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Submitted (13-027-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research: 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, 741:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: Kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MT024
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pl, TAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 3. II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 82360)
Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
Direct Submission
                                                                                                                                                                                                                                                                                 1090 TTGGATCCTCCAATTCCACTTAATTATTTTGGTAACTGCAATGGGAGACATTGTGAGACT 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1207 AGTGATATGGTCAAAGGGATCGATGCGGATGCCATTGAAGCCAATGATGATAAGGTTTCA 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTATCGGAATCTAATGGAATCCCTTCAAAAGATTTCTCGGGATTACCGGATCGCCTAAG 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACCTCT 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGATTATGCAGAATTGATTTATGTGATTCAGTCCAGGGATTTTGAAAAAGGTGTGGAG 1337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGGAGTATCATTGCCTAAGATTCATATGGATGCATTTGCAAAAATCTTTGAAGAAGG 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               structural analysis of Arabidopsis thaliana chromosome 3. II Sequence features of the 4,251,695 bp regions covered by 90 and BAC clones
  GTCGTATCAGAGGAA
                                                  970 GIGITITGTITGCAIGGCIAAAGCIAAATTAGCCAAAAGCCAAAACTGAAGCIGAAGCTGCA
                                                                                                                                                                1030 GCAGGTAATGATGAAATTAAAAATATTATTGTGGGATTCACTGCGGATTATAGGAGCCGT
                                                                                                                                                                                                                           CTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCGTCATGCGTTGCAAAA
                                                                                                                                                                                                                                                                                                                                                                       GAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1387 ATAGATAGGACACAAGCCAFCTCTTTGGCAGAGAAGAGAGAGAGGAGGAGGAGGCGGCGTTGAG
                                                                                                             TCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGACTT
                                                                                                                                                                                                                                                                                                                                            GCAACACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGA
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Arabidopsis thaliana
Eukaryota; Viridialantae; Embryophyta; Tracheophyta; Sp
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arbuu666 82360 bp DNA PLN Arabidopsis thallana genomic DNA, chromosome
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  GTATGGACATGCATGGTCAAATCAAAGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 7 (3), 217-221 (2000)
20363099
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VERSION
KEYWORDS
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RMRKRKGTPELVAALLHUTFPCLLEPPAPKVIMKLVOTKLGWKISYSTALRGEROAVO
DLKGSAEDSYKDINCYLYMLKKVNEGTVTIKLDESCKFQYLFIALGASIEGFQAMRY
VILLDATHIKKVSMYSRYSRFHGIRERVRNSRTYLVPDRSQMDIPDDIKALKVPL
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24898.234981)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codou_start=1
//evidence=not_experimental
/protein_id="BAB01195.1"
/db_xxef="c01:1994166"
/translation="MAPRTIPPLKKRKGVAGGTKPIDVVTKATTEPPTTTEEPSATE
EXPERENCE/CONTRACTOR TO THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FHMPRDPNHRLMGMWMLLERTARIERKKEACIIIAPIKTGDKAPQVDEFCLKAVSDLT
FCRRCQMGRYFEDYMLGTISHTVNHPRGSVPNNEKYWSVGFCLPRELLAFAIPOL
RETFMEDIAGADEGCPRMCKVRFKKNHLKGFPLDTIYAELGITQRRKESRLIRFDEIY
QQDIQALQIATAGPKFRPDPPAVGQGELSVSVVENIENDKRWDQLNEIITMIS
DLDKRYESLEAFKDIAGAGEBRNQGERGESVSVVENIENDKRWDQLNEIITMIS
QCKDGYPKEKDPKEKDGRAEERKNQESMQEKDGDPIEKDGYQEKDGOGEBGGVPKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELMRMLPPGPTVRWSVEDGEDRSSDGMDREKCSRKHKDKCIRTHPRIAHGCNLTGKGR
KHQEWVRNVIHHIGSISRLPSCIYLLSHGETDRRSVRPNGDSMDNQRESPRWEPMDKT
DVGHASKPKADGRRISWASLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MDRLCESDPWYDEMKSAKRIMQQLEEVAMMEEIPIICPCGGRIL
DIISEKDGDKGKRYYECTDYKNDGLHIQKLMDKAMVEEVNRLREQVDNHHQKIQSLEY
SNQEVLSEFDBIQKKMGTLMRVRNYWVCYYRQVFHCILSIPLYSQFSLVFSVLSLNL
                                                                                                                                                                                                              /translation-"MMRMSVSIYLQELSRVEVVNKSSIGKNYADLGSNEDEMRDYATI
VMGELEGQGTEQNEVIVEVDDTQDPEIGSRDDRDDDDRGDEYVEPPAVESSQFKKEW
EDSISLTLREEFPSRAALHEVVDKGAFANSFGYVIKKSDKERRYNKMHTCTRISKSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"mveertkilsrknekdqaepastdpagwsqqltlelvdygssrv
krclqqkhfpapyiredaqgladhlttsrhhktplkvsqhiskllvgkgvrlgeynst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(26878, .27120,27210, .27491,27693, .27854, 27950, .28175,28419, .28702,29026, .29487))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(25891. 26085,26155, .26349,26412, .26534)
/note-"contains similarity to Mutator-like transposase
gene_id:MT024.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(33399, .33608,33762, .33830,34025, .34098)
/note="gene_id:MTO24.10
unknown protein"
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join(34168. 34242,34530. 35934,36128. 39479)
/note='gene_id:MT024.11"
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39663. 40357
/note="gene_id:MT024.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strong similarity to unknown protein"
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/protein_id="BAB01193.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
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/db_xref="G1:11994165"
                                                                                     /evidence=not_experimental
/protein_id="BAB01192.1"
/db_xref**G1:11994163"
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/codon_start=1
/pseudo
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GEGKGFITANETLTGWNVGLCPENIEKNMLLPFEAFRRAEGROMSGVAGSTRLGIVG
SDFGWGFVPWCIVTIDKDASVSLSESGGGSGGVEVGVCLKKDDVERFGSLFSIGLE"
Join (21572. .21604.21666. .22063,22148. .22642,22710. .22929)
/note="contains similarity to Mutator-like transposase"
                          GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
Genes encoding tRNAs are predicted by tRNAscan-SE
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MWE13 and the 3' clone is T13110.
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/evidence=not_experimental
/poteain_id="Bab0iju0.1"
/db_xref="c1:1)994161"
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SSETWESIGKPDEHFAGFIYUNGEIKLVVBFLEIIDKLVLSKESNPPFKKTLNNDGEV
SKDLIREVPVIMESITVNGFHVLPSQVEFWRIFEKHPDVAKEFFPNNIVKTANNDGEV
SKDLIREVPVIMESITVNGFHVLPSQVEFWRIFEKHPDVAKEFFPNNIVKTAMNY
LLSLIFTLRQSPREISKNDLDGACGLLRSMKEAGFKLDWLEKKLNEVLEKKEKEESYE
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/db_xref="G1:11994162"
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LFYHVPELTFRSLISKLKSSLSATLHYLPLAGRLVWDSIKTKPSIVYSPDDKDAVYL
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HHAVLDGKTTAMFLKAWAHNCKQEQEALPHDLVPSLDRIIVQOPTGLEFKLLHWISA
SNNKPSLKLFPSKIIGSDILRVTYRLTREDIKKLRERVETESHAKQLRLSTFVITYAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence-not_experimental
complement(join(10964. .11326,11419. .11702,11802. .11968,
12054. .12160) /
/note-"emb|CAB68159.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence-not_experimental
/product-*retroelement pol polyprotein-like"
complement(joln(9270, .9952,10067, .10153))
/note-*contains similarity to copia-like retroelement pol
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/product-"anthocyanin 5-aromatic acyltransferase-like

    82360
    Organism-"Arabidopsis thaliana"
/strain-"Columbia"

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complement(12716. .13195)
/note="emb|CAB38296.1
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http://compbio.ornl.gov/Grail-1.3/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MTO24"
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5793. . 18151
/note="gene_ld:MTO24.1"
/codon_start=1
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RGKREAANDIRGTPEEGFRFVDYYMYMLQKMNHESGSYVEVDEENKFNYLFFALGSSI
                                                                                                                                                                                                    EGFRLMRKVI I LDGTHMKTAYGGI LIVATTQDPVHSRCASPWECARAYTEAEFLRCYF
GGEKYNRDTSNSVESVNGVLEKVRNYSLLQL I DAI VGKI AEWFAKHRKSLEL I PSGQY
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                                                                                                                                        /translation="MKRNVDETSTKLKVSYFPFSFQGRKLRPNYIRDNEDLECYFEDV
                                                                                                                                                        NEEGFRSILHVESNMRMNENERFDKILREDLVRQNVNNEDTSLIVGTDEIGGAVLAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16329 CCGCCCCCCCCCGGGATTCAATCAAACCAAA---CCATCCATTGTCTATTCTCCTG 16273
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                                           to Mutator-like transposase
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              .50400,50660.
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                                                                                                                                                                                                                                                                                                                                                                                                        CTGTTATCCCTAATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTA 246
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              .49959,50068.
                                                                                                                                                                                                                                                                                                                                          Score 71.8; DB 13;
Pred. No. 1.7e-07;
0; Mismatches 627;
                                          /note="contains similarity
/evidence=not_experimental
                                                                                         /evidence=not_experimental
/protein_id="BAB01196.1"
/db_xref="G1:11994167"
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            .49683,49880.
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unknown protein"
                                                            gene_id:MTO24.13"
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llarity 46.2%;
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brassicacles; Brassicaceae; Arabidopsis.

1 (bases 1 to 341064)

Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Ronning,C.M.,
Koo,H., Fujii,C.Y., Utterback,T., Barnstead,M.E., Bowman,C.L.,
White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana 'IGF' BAC 'F27B9' genomic sequence near marker
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                                                                                                                                                                                                                                     CATCAGACTTTCGGTCACGGTTAAACCCTCCGTTACCGCCGACGTTCTTCGGGAACTGCA 15604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15543 AAGGTTTCATCACGGCGGTGGAGACTTTGACCGGATGGGTCAACGGATTGTGTCCCGGAGA 15484
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                                                                                                                                                               CAGCGGATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTC 1017
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* NOTE: This is a "working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is a rbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
898 ATGACGTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTA
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Arabidopsis thaliana chromosome 1 clone IGF-F27B9,
IN PROGRESS ***, 5 unordered pieces.
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HTG; HTGS_PHASE1.
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Town, C.D. and Kaul, S.
Direct Submission
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                                              14022: contig of 14022 bp in length 14072: gap of unknown length 35113: contig of 21041 bp in length 35163: gap of unknown length 86858: contig of 51695 bp in length 86908: gap of unknown length 170536: contig of 83628 bp in length 170566: gap of unknown length 170566: gap of unknown length 170566: contig of 170478 bp in length.
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46.2%; Pred. No. 1.9e-07;
tive 0; Mismatches 627;
                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                    /clone="IGF-F27B9"
59862 c 59862 g 110479 t
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170536:
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Asamizu, E., Sato, S., Kaneko, T., Nakamura, Y., Kotani, H., Miyajima, N. and Tabata, S.
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e; eurosids II;
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                                                                                                                                                                                                                                                                                                                        66062
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Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MXF12.
AB016892 BA000015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAAAGCCTGCAAAATTTGACATTACCTCTGTTGATTATGCAGAATTGATTTATGTGAT
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ATGACGTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTA
                                         -----Greacccearrerererecerrie
                                                                                         CAGCGGGATTGCCGAGGACITCTGACGCCCCGTGTCCGCCTAACTACTTTGGCAACTGTC
                                                                                                                                  65883 CATCAGACTTTCGGTCACGGTTAAACCCTCCGTTACCGCCGACGTTCTTCGGGAACTGCA
                                                                                                                                                                                1018 TTG------CGTCNTGCGTTGCAAAAGCAACACATAAAGAGTTAGTTGGGGATAA
                                                                                                                                                                                                                                                                                                                                                                      AAAAGGCGTTCTTGCAGATGCAAAAACTTGGTTATCGGAATCTAATGGAATCCCTTCAAA
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                                                                                                                                                                                                                                                                                                                     AAGGTTTCATCACGGCGGTGGAGCTTTGACCGGATGGGTCAACGGATTGTGTCTCCGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                    66063 ATATAGAGAAGAATATGCTTTTACCGTTTGAAGCGTTTAAGAGGATGGAACCGGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGATTTCTCGGGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATG
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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Nakamura,Y.
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FEATURES

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/evoidence-mort_experimental
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/product="ABC transporter-like protein"
/product="ABAB10828.1"
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/db_xref="G1:1017549"
/translation="MGNKKLLTGGSSKTHGSGSSYRDPLLQNQEDKPKANGSENGLND
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GGNIIDTVSRDVKTPEQGPSELLANRAVVIILLIVVIGSICTALRAWLENSSERVV
ARLIKDLFRHLMHQEIAFYDVTKTGELLSRLSEDTQIIKNAATTNLSEALRNVTAALI
GVGFWFTSSWKLTLLALVVVPVISYANKQFGRYLRELSHTTQAAAVAASIERSFGA
VRTVRSFAKESYMVSQYSKKVDETLKLGLKQAVLUGLFFGGLNAAFTLSVITVVSYGA
YLTTYGSMYVGALTSFIILSTLVYGSSVSSLSSLYTTAMKAAGARRRPPGILDRVSSMS
SGGDKCPVGNPDGDVELNDVWFAYEDSRPSHMILKGTSLRLFPGSKVALVGPSGGGKTT
IANLIERFYDDLKGKILLNGVSLMBISHQYLHKQISIVVGEPILFNCSVEENIAYGFD
GBASFTDIENAAKMANAHEFIRAFPDKYNTVVGERGLRLSGGCKGRTA
GRASFTDIENAAKMANAHEFIRAFPDKYNTVVGERGLRLSGGCKGRTA
GBASFTDIENAAKMANAHEFIRAFPDKYNTVVGERGLRLSGGCKGRTATARALLTNPS
VLLLDEATSALDARSESEYLVQDAMDSLMAGRTVLVIAHRLSTVKTADCVAVISDGEVAE
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GTGLATFVVVLMLMMRQMKRKNRKEBRVVMFKKLLNMYTYAELKKITKSFSYIIGKGG
FGTVYGGNLSNGRKVAVKVLKDLKGSAEDFINEVASMSQTSHVNIVSLLGFCFEGSKR
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ONILLDGUCPRVSDFGLARKLCEKRESVLSLMDTRGTIGTYAPEVFSWAYGRVSHKSD
VYSTGMLVIDMIGASKEIVETVERVDSAASSTYPPDWIYKDLEDGEQTWIFGDEITKEER
EIAKKMIVVGLWGIQPCPSDRPSMNRVVEMMEGSLDALBIPPKPSMHISTEVITESSS
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THMHRVAVKTGKREPENPKSLKLLWSPEIGPDVFRYTLINTREDIGKLRERLKKES
SLSSVSSSKELRLSTPVIVSYALICLIKARGGDSPRYGYGFAVDGKSLWVPPPS
SYFETPMSEEGFLAARRWVSDSVEALDENVALKIPEILEGFTTLSPGTQVLSVAGSTR
                                                                         TVYRGNLSNGRTVAVKVLKDLKGNGDDFINEVTSMSQTSHVNIVSLLGFCYEGSKRAI
ISEFLEHGSLDQFISRNKSLTPNVTTLYGIALGIARGLEYLHYGCKTRIVHFDIKPQN
                                                                                                                                               ILLDDNFCPKVADFGLAKLCEKRESILSLIDTRGTIGYIAPEVVSRMYGGISHKSDVY
SYGMLVLDMIGARNKVETTTCNGSTAYFPDMIYKDLENGDQTWIIGDEINEEDNKIVK
KMILVSLWCIRPCPSDRPPMNKVVEMIEGSLDALELPPKPSRHISTELVLESSSLSDG
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WTQEEKNILPKNSDNASFSSVVSYKEESGIPQVPYMTARIFRSDFTYSPPVSPGWKFL
RLYFYPTSYKSGFDAVNSFVSVTVNDFTLLQNFSADLTVKASIPESKSLIKEFIVPVY
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NQMAREEMDVIRLSGGPRIPIYLDFRIYVGSESGPRPDLRLDLHPLVKDNPEYYEAIL
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VHRLNVGGHMVDEVNDSGMFRRWLSDDYEFLIGGVSPYMPDVNISYTEKTPAYVAPAY
   SGVEILKLNDSDGNLARPNPELLVSTDSTPDDSNVTPPIKGKPHVLVIILIVVGSVIG
                                          LATFIVIIMLLIRQMKRKKNKKENSVIMFKLLLKQYIYAELKKITKSFSHTVGKGGFG
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/protein_id="BAB10829.1"
/db_xref="G1:10177550"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="receptor protein kinase-like protein"
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/db_xref="G1:10177548"
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/note="gene_id:MXF12.8"
/codon_start=1
/pseudo
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join(25348. .26359,26401. .26756)
/note="gene_id:mXF12.7"
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                                                                                                                                                                                                                                                                                                       10819. .13239
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                                                                                                                                                                                                                                                            QEAEKQTQTLDSTII"
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                       product or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.lastate.edu/gui-bin/sp.cgl). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is KISE6 and the 3' clone is KISE6.
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RWTVTESGDIJLSSNLVNASFTSEASKOKAGVSEI PYRKARIFRSEFTSFPVFPGSIF
LRLYFPPTOVEKSGEDANUSFFSVKNGFTLLENNFNADSTVQASIPLSNSLIKEEIIPV
HQTLNLTFTPSKNLLAFVNGIEIVSMPDRFYSKGGFDNVLRNVSSDVDFQIDNSTAFE
SVARLANGGQTVNEVDDSGMFRRALSDSFVSKGSIVNVFVRINTSTFPRYPAYD
VATSRLMGNSSNLAFNLTGARLITVDAGVTVLVRLHFCETLEVOVTKAGORVFSIFVED
KMAKKETDVIRLSGGPRIPMYLDFSVYVGFESGMIQPELRLDLVPLKDTNOTYYDAIL
proteins in the databases are described in
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SYSRNWTABROKILSSNLVNASFTAGASYQESVADIPVMAALRERSEFTYSFPVTPG
SYSRNWTAPPTRYGGORDAN KFFSVKVNGFTLLINNFSADLYVKASKPOTEFIIKEFI
IPVYQTLNLTFTPSLDSLAFVNGIEIVSIPNRFYSKGGFDDVIINVGSSVDFHIENST
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GMSYRDPGTSNRTVVMGRAKIRLSPLMTSYKERPISGGIDLVGLNSDQCVVKKGYLTY
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/protein_id="BAB10826.1"
/db_xref="GI:10177547"
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/protein_id-"BAB10824.1"
/db_xref-"GI:10177545"
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/db_xref="G1:10177546"
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/note="gene_id:MXF12.4"
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/chromosome="5"
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Genes with similarity to
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; admonlophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaee; Arabidopsis.
                                                                                                      Lin,X., Raul,S., Town,C.D., Benito,M., Creasy,T.H., Ronning,C.M., Croo,H., Puji,C.Y., Utterback,T., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana 'IGF' BAC 'F7F7' genomic sequence near marker
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                                                                                                                                                                                                                                                                                                                                                      Submitted (11-10N-2000) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org on Jan 19, 2001 this sequence version replaced gi:12280790.

* NOTE: This is a "working draft" sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
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Pred. No. 3.2e-05;
0; Mismatches 520; Indels
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/db_xref="taxon:3702"
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Town,C.D. and Kaul,S.
Direct Submission
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Best Local Similarity 45.11
Matches 436; Conservative
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IFYRIINVTRPFFDSVIVPNLKTSLSSCLSHYLPLAGKLIWEPLDHKPTIVYSQNDDV
SFSVAETNADFSSLSGNEPFPSTELYPLVPALQSSDDSASIVSFQVTLFPNQGFCIGV
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SFTKILAGGKEPANPKSLKLNPSFEIGPDVVRYTLQLIFREDIGTLRREHLKREVSSSS
STSSKELRLSTFVIVYSYLVUCITRRGGEPHRPVGYAFSVDCRSLMNPPTPNYFGN
CIAGCSRMMITAKMFGEEGLLAAATWVSDSIEGMDESFAWKIPDFTAYATLPPETQL
ILVSGSNRFGVYELDFGWGRPDKVWVVSISPGNGISMAESRDQNGSVEIGFSLKKHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1248 GGAAAGCCTGCAAAATTTGACATTACCTCTGTTGATTATGCAGAATTGATTTATGTGATT 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACGAA 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               948 TTCAGTTTTACAGCGGATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTACTTT 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/product="anthocyanin acyltransferase-like protein"
/protein.id="BAB10830.1"
/db_xref="G1:10177551"
                      /product="transposase-like protein"
complement(join(30804. 30874,30947. 31289))
/note="contains similarity to Ac-like transposase
gene_ld:MXF12.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAACTGTCTTGCGTCATGCGTTGCAAAAGCAACACATAAAGAGTTGGGGATAAA
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Pred. No. 1.4e-05;
0; Mismatches 223;
  /evidence=not_experimental
                                                                                                                                                                                               /evidence=not_experimental
                                                                                                                                                                                                                        32432. .33823
/note="gene_1d:MXF12.10"
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HTG; HTGS_PHASE1.
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Arabidopsis thaliana
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Best Local Similarity 49.4%;
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Burnitted (09-JUN-1999) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarzu, Chiba 29-0812, Japan (E-Bant); Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (sites)
Stancko,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
BNA Res. 7 (3), 217-221 (2000)
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:MOD1
AB028618 BA000014
                                                                                                                                                                                                                    28386 CGGTCCGTTTCATGTATGCTGCTGATTTCAGGAACCGGTTAGATCCACCGGTTCCTGAGA
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                                                                                  GCCAACGCGTATCTTTGGACATGCTTGGTAAAGACGCGTGGAGGA--GATGAGAACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGAGAAGATGGTTTGTTAATATGGTCGAAATTCTAAGTGATTCGGTTAGAAGTATTG
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                                                                                                                                                                    TCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTA
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The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.orni.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://crambio.orni.gov/Grail-1.3/), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is Ti31lo and the 3' clone is T26G12.
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VVBSRDFSTSTSKELRLEFELPRLVPLDVPELQVSSDSASLISLGJTLFPROGFSIGTVH
HVVBGGKTASKFHKSWAHICKHGTTPQDFDLPTVLDRTVINVPAGLEGKIFQLISSYIS
EEKDYARTLTLPPAKEIDNDVVRVTLELTEVDIEKLKERAKNESTRSDLHLSTFVVSY
AYULTCWKKGGGDARRPYRMAADPRINLDPPVPLTYRGKOVLPIDFNGYRATTFL
GKDGYVNGVBILSDSVRGLGSRNIBSIMEVYEDGTRAMKLDYQNVYTGSNGFIYED
DFGWGRPVKTDVMSLYKNNBFSMSARRDEIGGLBISISLKKCEMNVFLSLFPFDFDIY
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VAAHHAVLDGKTSSTFIKAWAQICKQELQSMPENLTPSYDRSLIKYPTYLDEKMIELV
RSLKEDQTNIRSLTSLPSSKLGDDVVLATLVLSRADIERLREQVKNVSPSLHLSTFVI
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FMEEKGFVTAAEIISDLVKGLSSRKIETIADTFVEGFSFQSWSTQFGTIAGSTRLGVY
EADFGWGRPVKVDIVSIDQGEAIAMAERRDESGGVEIGMCLKKTEMDSVVSFFNNGLH
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VFFYELTESTRDHFHSIILPKLKDSLSLILRNYLPLTGHITWEPNEPKPSIIVSENGV
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/product="anthocyanin 5-aromatic
acyltransferase/benzoyltransferase-like protein"
/protein.id="BAB02518.1"
/db_xref="GI:11994477"
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/product="anthocyanin 5-aromatic
acyltransferase/benzoyltransferase-like protein"
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/note="contains similarity to unknown protein
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/note="gene_id:MOD1.5
'unknown protein'
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similarity are described
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/clone_lib="Mitsui P1"
2123. .8637
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/note="gene_id:MOD1.3"
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/codon_start=1
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/db_xref="GI:11994478
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gene_id:MOD1.2"
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16407 TGAGTCAGGTGGCGTTGAGAATGGGATTGAAAAAAGACTGAAATGGATTGGTCTTTGAAAAAAGACTGAAATGGATTGGATGGTTTGAAAAAAAGACTGAAATGGATTGGACTCT 16466
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	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	113	81 81 81 81	0.000	936 936 936	22 22 22 22 22 22 22 22 22 22 22 22 22	AAF58254 AAF58257 AAF58259 AAF58262	
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Oligonucleotide D1
Oligonucleotide D2
Oligonucleotide D2
Oligonucleotide D2
Oligonucleotide D1
Oligonucleotide D1
Oligonucleotide D1
Oligonucleotide D2
Chicken D2
Chicken D3
Chicken D4
Arabidopsis thalia
Arabidopsis Halia

ALIGNMENTS

Oil seed rape cyst DNA encoding a hum Human PRO1063 cDNA Membrane-bound pro

Juman PRO4063 (UNG

Mouse Wnt-3a gene. Murine Wnt-3a enco Macromolecular sys

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Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Petilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
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                                                                  Aromatic acyl transferase coding sequence.
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                                                                                                                                                      Location/Qualifiers 67..1413 /*tag= a
                                                                                                                                     Petunia hybrida (Clone pPAT48)
                                                                                                                                                                                                                                                                  95JP-0046534.
95JP-0067159.
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                                              (first entry)
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17-FEB-1995;
29-JUN-1995;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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(SUNR) SUNTORY LTD

Arabidopsis thalia Arabidopsis thalia

AAT37310 AAC48422 AAC47537 AAC48421 AAC48416 AAC48640 AAC48415 AAC3553 AAC3254

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                                                                                                             Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                         plants
tone,
                                                                                                                                                                                                                                                                                                                                             ttatccatggcaggtgaagtagcaaaacaagaagttacaaaagtgaaagtcctgaaaaa
                                                                                                                                                                                                                                                                                                                                   ACAAACGTGAAACCACATAAACCACTAGGAAAAAAAGAGTGTCAATTGGTAACATTTGAT
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Nakao M, Tanaka Y, Yonekura K;
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     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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TTTGATGGAATGGTGTATTTGTACCAAGGCAAAATGGAGGAAGAAGCATTGATGTGGAG
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gacgggacatccacgtggcattttatgagctcatgggccgagatctgtcgtggagcccaa
                                  814 GACAAAATCAAGTCAACAGTCAATGCCAACTCAGGAGAG------ACGCCATTCTCC
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                                                                                                                         CCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAAGTTCTCCGAGTTAGCAATT
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31 - AUG - 1999;
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CAGTACAAAGATGCTGGAGTGAACTGTGTTGCTGTTGGAAGTTCGCCAAGGTTCAAGGTT 1224
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       534 ccggaggacataactattctcaccgtcttcgccgactgtcgccgccgcggttgatcctcca 593
                                                        1045 TTGTTACTAGCAAGCCCGATCGAGTTCGCTGGTGGGATGATACAACAAGGGATCGTGAAG
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990S-0131449.
990S-0132449.
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PR 23-JUL-1999; 99US-0145214.
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PR 23-SEP-1999; 99US-0153018.
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778 aaagcaggaggcataagtattgatgtggagataactcttgaagcttctgttatggagaag 837
                                                                                                                                                                      control;
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                                                                                                                                                                                        metabolic pathway; promoter; termination sequence; ss
                                                                                                                                                   Arabidopsis thaliana DNA fragment SEQ ID NO: 58217
                                                                                           BP.
                      1375 TTGGAGAAGATAAAGAGTT 1394
                                                                                          AAC48640 standard; DNA; 1364
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9905-0130891.
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99US-0139452
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99US-0138094
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                               838 cttgtgaagagcaaagagtt
                                                                                                                                                                                                          Arabidopsis thaliana
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                                                                                                                                                                                                                                                                    25-FEB-2000;
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16-JUN-1999;
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30-APR-19
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Pred. No. 1e-78;
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99US-0160980.
99US-0160981.
99US-0161404.
99US-0161405.
99US-0161360.
99US-0161360.
99US-0161361.
99US-0161361.
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          22-0CT-1999;
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TGATGAAGAAGGCACCACAAATTGCAGGACTTGATTCCTTGTAATAAAATCTTGAATTT 482
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Pred. No. 1.1e-24;
0; Mismatches 500; Indels
99US-0148565.
99US-0148684.
99US-0149368.
99US-0149175.
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99US-0159637.
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9905 - 0160814
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CTCAGGAGAGGCCCATTCTCCACATCCAATCACTCCCGCACGTGTGGCTAGCCGT
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                                                                                                          AACCAAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCTCAACCATCAGATGCACCGA
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                            CATGGGATTAGCATTTAACCATGCTGTGCTGGATGGTACTTCGACGTGGCACTTTATGAC
                                                                                       cgcatggtccgaaatcttccaaggacaagagagacaaccaaaacgatgacttgtgtcttaa
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.

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990S-0154018.
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Matches 283; Conservative
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   GATGAAGAAGGCACCACAAATTGCAGGACTTGATTCCTTGTAATAAAATCTTGAATTG
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                                                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 34861
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                                                                                                                                                                                                                                      1160 TCTTTCAGTACAAAGATGCTGGAGTGAACTGTTGCTGTTGGAAGTTCGCCAAGGTTCA 1219
                                                                                                                                                                                                                        ATAGGTTTGATGGAATGGTGTATTTGTACCAAGGCAAAAATGGAGGAAGAAGCATTGATG 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                               1201 cggctcatcaagacgggaggattcgtagcgttgtggcggattgggaagcgaatcccaggt 1260
1040 CAGGTTTGTTACTAGCAAGCCCGGATCGAGTTCGCTGGTGGGATGATACAACAAGCGATCG 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                            1141 cggcagaggttttgtcacgtgatcttaaatggtgcgctgatcagcttaaccagagtgttg
                                                       1100 TGAAGCATGACGCTAAGGCCATTGATGAAAGAAACAAGGAGTGGGAGAGCAACCCGAAGA
                                                                                                                                                                                1220 AGGTTTACGACGTGGATTTTGGATGGGGAAAGCCAGAGAGTGTGAGGAGTGGTTCGAACA
                                                                                                                                                                                                                                                                               1340 TGGAGATTAGTTTGGAAGCAAATGCTATGGAGAGGTTGGAGAAAGATAAAGAGTT 1394
                                                                                                                                                                                                                                                                                             Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.0%; Score 81; DB 22;
Best Local Similarity 1.1%: Pred. No. 2.3e-10;
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               920 TCAAGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGTTGATC 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          860 TCTCCACATTCCAATCACTCTCCGCACGTGTGGCTAGCCGTCACACGTGCGGCGCCAAC 919
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99US-016140S.
99US-0161369.
99US-0161360.
99US-0161320.
99US-0161993.
99US-0161993.
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990S-0151438.
990S-0151930.
990S-0153070.
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990S-0150566.
990S-0150884.
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990S-0155139.
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Matches 267; Conservative
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12-0CT-1999
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25-OCT-1999;
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27-AUG-1
27-AUG-1
27-AUG-1
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31-AUG-1
01-SEP-1
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                 Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                   TGGGAGAGCAACCCGAAGATCTTTCAGTACAAAGATGCTGGAGTGAACTGTGTTGCTGTT 1200
                                                                                                                         GTGAGGAGTGGTTCGAACAATAGGTTTGATGGAATGGTGTATTTGTACCAAGGCAAAAAT 1320
                                                                                                                                                           1321 GGAGGAAGAAGCATTGATGTGGAGATTAGTTTGGAAGCAAATGCTATGGAGGTTGGAG 1380
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Gaps
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Conservative 322; Mismatches 197; Indels
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17-MAR-2000; 2000US-0190259.
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                       The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                     5.0%; Score 81; DB 22; L ilarity 1.1%; Pred. No. 2.3e-10; Conservative 322; Mismatches 197;
                                                                                                               Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
Example 6; Page 127; 159pp; English.
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                                                                                         monitoring gene expression.
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Matches 6; Conserv
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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gene expression; ss.
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illarity 1.1%; Pred. No. 2.3e-10;
Conservative 322; Mismatches 197
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24-APR-2001 (first entry)
                              Oligonucleotide D2004
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
.3e-10;
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6; Conservative 322; Mismatches
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                                                          (CLIN-) CLINICAL MICRO SENSORS INC
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             99US-0145695
2000US-0190259
                                                                                                                      WPI; 2001-159728/16
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Best Local Similarity
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             26-JUL-1999;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                                ETM; mismatch; genotyping;
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                                                                                                             AAF58262 standard; DNA; 936
                                                                                                                                                                                                                                                                                                             26-JUL-2000; 2000WO-US20476.
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17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monitoring gene expression
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gene expression; ss.
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Matches 6; Conservi
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Search completed: November 5, 2001, 18:11:37 Job time: 15432 sec

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AB026495 Petunia x
AB002244 Arabidops
AB008264 Arabidops
AL137189 Arabidops
AB002249 Arabidops
AL13421 Arabidops
AF002109 Arabidops
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2787.883 Million cell updates/sec
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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G37798 GARP Plasmo
J03998 Plasmodium
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AC005507 Plasmodiu
AE001366 Plasmodiu
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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PN JP 1997070290-A/3
PD 18-MAR-1997
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 196915
MASHIRARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashlkari,T., Tanada,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Ashlkari,T., Tanada,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070290-A 3 18-MAR-1997;
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E12755.1 GI:3251587
JP 1997070290-A/3.
unidentified.
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1. .1605
/organism='Petunia hybrida
                         /tissue_type='petal'
/clone='pPAT48'
67. 1413
/product='acyltransferase'
                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                        Score 1603.4;
                                                                                      Location/Qualifiers
1. 1605
/organism="unidentified"
/db_xref="taxon:32644"
a 318 c 376 g 434
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                           Pred. No. 0;
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GLAFNHAVLEGTSTWHFWTSWSELCGGSTSISVPPFLERTKARNTRVKLNLSQPSDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                  EHAKSATNGDVPANVDPPLRERVFKFSELAIDKIKSTVNANSGETPFSTFQSLSAHVW
LAVTRARQDLKPEDYTYYTVBADCRRRYDPBMPESYFGNLIQAIFTVTMAGLLLASPIE
FAGGNIQQAIVKHDAKAIDERNKEWESNPKIFQYKDAGVNCVAVGSSPRFKVYDVDFG
WGKPESYRSGSNNRPDWYLYQGRNGGRSIDVEISLEANAMERLEKDKEFLMETA*
318 c 434 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAAACGTGAAACCACATAANCCACTAGGAAAAAAAAGAGTGTCAATTGGTAACATTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCCTTACCTAGCTTTCTA/TTACAACCAAAATTTCTCATCTATAAAGGTGCTGAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGATGAAGAAGGCACCACCACCAAATTGCAGGACTTGATTCCTTGTAATAAAATCTTGAAT
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Submitted (21-APR-1999) to the DDBJ/EMBL/GenBank databases
                                                                            Yoshikazu Tanaka, Suntory Ltd., Institute for Fundamental Wakayama-dai 1-1., Shimamoto, Osaka 618-8503, Japan (E-mail:Yoshikazu_Tanaka@suntory.co.jp, Tel:81-75-962-8807 Fax:81-75-962-8262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGAAGGGCTTCATCGCCCTCTTCTAGCTGTGCAGCTCACCAAGCTCAAGGACGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonym:Peunia hybrida"
                                                                                                                                                                              /organism="Petunia x hybrida"
/db_xref="taxon:4102"
Unpublished (1999)
2 (bases 1 to 1605)
Tanaka,Y. and Yonekura-Sakakibara,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1603.4;
Pred. No. 0;
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0; Mismatches
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1. .1605
                                                                                                                                                                                                                                       /gene="PA148"
67. 1412
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                                                                                                                                                                                                                                                                                  /gene="PAT48"
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99.9%;
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Fujiwara,H., Fukui,Y., Toshihiko,A., Yamaguchi,M. and Kusumi,T.
Molecular cloning and blochemical characteization of
hydroxycinnmamoyl-CoA:anthocyanin
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homolog, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTITIATITATGAGCTGCTATGACTCACATGCATGTATGTTTATTTTTGGAGGGGT
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                                                                                 GTCACACGTGCGCGCAACTCAAGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGAT
                                                                                                TGGGAGAGCAACCCGAAGATCTTTCAGTACAAAGATGCTGGAGTGAACTGTGTTGCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB026495 1605 bp mRNA For acyltransferase hab026495. 1 GI:7415598 acyltransferase hab026495.1 GI:7415598 acyltransferase homolog.
Petunia x hybrida cDNA to mRNA.
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1321 1381 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

AB026495 LOCUS

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        ACCTCGTGGTCCGAGCTTTGCTGTGGGTCCACCTCAATTTCTGTCCCACCATTCCTTGAA
                                              661 CGAACCAAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCTAACCATCAGATGCACCC
                                                                                                                                                             841 AACTCAGGAGAGGCGCCATTCTCCACATTCCAATCACTCTCCGCACACGTGTGGCTAGCC
                                                                                                                                                                                                                             GTCACACGTGCGCGCCAACTCAAGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGAT
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On Sep 15, 2000 this sequence version replaced g1:2264316.

Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MRO11
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein.'

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/),
(Enformatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/),

GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),

MetGene2 (S.M. Hebsgaard, et al., CBS Technical University of Denmark, http://www.cbs.dtu.dk/services/NetCene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).

Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE).

This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.

The 5' clone is MOM1 and the 3' clone is MZPI8.
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/protein_id="BAB10046.1"
/db_xref="GI:10176840"
/translation="MYTLHPHYQQDEQQQQBEARYEWDLSLSTVVSSSSSASDVIG
AIEFDPAINTATALSRKIRPYGLPSELLRNNAVSGTGVSFVDQATACEYYICTPAKL
SSLRWRPGSGGRVIGSGDYDGVVMEYDLEKRTPVFERDEHGGRRVWSVDYTRHGGAST
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GYVYDIRKLVDPALTLQGHTKTVSYVRFLDGGTVVTAGTDGCLKLWSVEDGRVIRTYE
GHVNNRNFVGLSVWRNGALFGCGSENNRVFVYDRRWGKPVWVDGFEPVGMNSGSDKRF
                                                                                                                                                                                                                                                                                                                   Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to photomorphogenesis repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato, S., Kotani, H., Nakamura, Y., Kaneko, T., Asamizu, E., Fukami, M., Myajima, N. and Tabatu, S.
Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned Pl clones
DNA Res. 4 (3), 215-230 (1997)
                                                                                                                                                                                                                                                                                                                                                        eurosids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura,Y.

Direct Submission
Submitted (02-JUL-1997) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                            genomic DNA, chromosome 5, Pl clone: MRO11
                                                                                                                                                                                                                          Arabidopsis thallana (strain:Columbia) DNA, clone_lib:Mitsui
                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sp
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSSVCWRQSGVDQCTLVAGGSDGVLQVYVGKRKP"
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/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                  Brassicales; Brassicaceae; Arabidopsis.
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2972. .4078
/note="contains similarity
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                                                    AB005244 B2415 bp
Arabidopsis thaliana ger
AB005244 BA000015
AB005244.2 GI:10176838
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                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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RESULT 3
AB005244/c
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                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                         ORGANISM
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TITLE
JOURNAL
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MEDLINE
                                                                                                                             ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                     KEYWORDS
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KTVDLRSLRPIPPPIRVKEYRLDEYIEVYHDGIGWRQGRVVKSEGGVMGSLFONWCTL
LLEATKKQLMFKQSDLRPLRVWEDGVWKTRESSLTQGSGDKTEVETCRKTFRKTLPR
NQMGSGNDSTLENENSNRKRRENLCSGSSVEETNILEEKKLPVWKILESMEVKTI
PQSPHERPLAEITENSREMLAVGMMLTFSCLLEQVRALQHDBARSSFISLSNSFAELE
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Join (2014). . 26228, 26308. . 26544, 26734. . 26827, 26932. . 27152,
77251. . 27384, 27507. . 27734, 28009. . 28416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(29073. .29168, 29422. .29523, 29617. .29795, 30379. .30495)
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pir ||T00970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(31483. .31584,31751. .31849,31964. .32145,32282. .32398)
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complement (join (19902. 19929, 20117. 20706, 20859. 20944,
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NNYFWVLFGLTQIFWSQIPNFHNWWLSLVAAIMSFTYSFIGIGLAGKIIENRKIEG
SIGIPAARMIGEKWAIVFGAGGIATAGTSTYSFILERQPARKGYMKKASTVA
VIGTFFFFCGGCGTAARGDAGWIAFSYSPSILLERQPIARGYMKKASTVA
SIGIPAARMICGKWAIVFGAGAGNIAFSYSPSILLIGEGDYTAGPAAGGTVUV
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EEPPWFSPGTIVELGSKRDBGEVVWVPALVYKEFKENDEYRYIVKDKPLIGRSYKSRPS
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LLSLVGSIYGLVGAKFG"
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vvSPSVGPHENPTITINLFGSASKNIPAGTLVYVAFRDGEFTGLLKTYNLCDVSACNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAEIEAGTNFELTLSDVLYVGYDEEIKYSVSLRRKTLEEEDPIIKMCVDFKVPAPAPA
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                                                                                           KLRIWEFVEY EKMIYLDGDIQVFKNIDHLFDTPRGYLYAVKDCFCEVSWSKTPQYKIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 CAGCTCACCAAGCTCAAGGACGGGCTCACCATGGGGATTAGCATTTAACCATGCTGTGCTG 573
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llarity 65.8%; Pred. No. 2.9e-79;
Conservative 0; Mismatches 292; Indels 12; (
                                                                                                                                                                                                                                                                                                         gene_id:MRO11.16
similar tc unknown protein"
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EEKKEEKKEEKKEEOKEEEPKK"
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ERVMLSQGRVWVSQGRVMGNLSQKCYIVLLEATKKQISFKQSDLRPLQVWEDGVWKLL
QYRESSLTQGSGDETSOSVRANNESDPPVTPRRGTTFPPLKQY BERTQRKTLERWQNA
SYNDSTRENDSED INKRKREESLCSDASVEDTTTPPLKQY BEKKLSIWKTLESVETVPQ
SPHFSPLVETREDCREMSAVGWMLTFPCLLEEVKSLQHDNSISSLISLSNNFCELEKH
GFNVKAPQSRISKLLSLRGKQSMKMDELKGAEKVTAEKESIKIENRFKILELGRENKEL
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complement(join(7690. 77884,7980. .8061,8178. .8265,
552. .8593,8938. .9139)
/note="contains similarity to remorin
gene_id:mR011.21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLPSPAPAEEKQEDSKAIVPVVPKEVEEKKEGSVNRDAVLARVETEKRASLIKAWEE AEKCKVENKAEKKLSSIGSWENNKKAAVEAELKKMEEQLEKKKAEYVEQMKNKIAQIH KEAEKREMERERAMIEAKRGEELIKARELAAKYRATGTAPKKLEGCM" complement(10928. .11128) //note="gene_1d:rRoil.20 unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(12199. .12825,12976. .13127,13189. .13258,
13376. .13819,13934. .13957))
/note="gb|AAC72114.1
gene_id:MR011.19
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complement(join(17869. .18087,18174. .18308,18396. .18719,
18960. .19283))
complement(join(5937. .6027,6112. .6201,6295. .6439,6693. .6793,6883. .6923,7005. .7016))
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TITLE
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Nakamura,Y., Sato,S., Kaneko,T., Kotani,H., Asamizu,E., Miyajima,N.
and Tabata,S.
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Arabidoposis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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                                              75123 GACCTCACTGCTCCCAAGGACCCCAACGAGACCTCCAACGGCGAA---GATGCTGCCAAT 75067
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                                                                                                  75006 CACACGATCAAGTCAAGTTCAGTAATCCCATCGGACAGTTCAAAACCCATTCTCA 74947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1284
                                                                                                                                                                                                                                                                                                                                                985 ATGCCAGAAAGTTACTTCGGCAACCTAATTCAGGCAATTTTCACAGTGACCGCGGCAGGT 1044
                                                                                                                                                                                                                                                                                                                                                                                                                 1045 TTGTTACTAGCAAGCCCGATCGAGTTCGCTGGTGGGATGATACAACAAGCGATCGTGAAG 1104
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               Structural nallysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned PI clones DNA Res. 4 (6), 401-414 (1997)
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Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MBD2.
AB008264 BA000015
AB008264.1 GI:2618500
                                                                                                                                               814 GACAAAATCAAGTCAACAGTCAATGCCAACTCAGGAGAG-----ACGCCATTCTCC
                                                                                                                                                                                                                                                                                                                                                                                 ATGCCGGAGGAATATTTCGGAAACTTGATTCAAGCGATCTTCACCGGAACAGCGGGGGG
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                                                                               CCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAAGTTCTCCGAGTTAGCAATT
                                                                                                                                                                                                              865 ACATTCCAATCACTCTCCGCACACGTGTGGCTAGCCGTCACACGTGCGCGCCCAACTCAAG
                                                                                                                                                                                                                                                                                 CCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGTTGATCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1105 CATGACGCTAAGGCCATTGATGAAAGAACAAGGAGTGGGAGAGCAACCCGAAGATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1285 TTTGATGGAATGGTGTATTTGTACCAAGGCAAAAATGGAGGAAGAAGCATTGATGTGGAG
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Nakamura, Y.
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AUTHORS
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Address for correspondence: **Sos@Razusa.or.jp
Address for correspondence: **Sos@Razusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?-wBD2
Genes with similarity to proteins in the databases are described
or product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),
MetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zcol.iastate.edu/Cgi.bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan.SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan.SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MJB21 and the 3' clone is MRD20.
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ATRKDWDGRELDGYLEEIEDIEPFKRNDDNTIHFTHEHNLSKDGTTLKKSILCVAC
VOLGTDTFYNCSESSCSFVLHETCANISKKRRHFLSPVPLVLCLQNQRNTETCNACQ
QVCCKGFIYSSFPKYVYREKFYDLQCSSITVPFFHGSHDHHLLFLKLKGRGNKYCECC
GIVQKEYAIGCTKCNYFLDFRCATLPLLVRLPRYDDHPLTLCYGDEKASGKCWCDICE
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SLPYSHPDEFIRTYESPILKERMFCFSSETIRMLKTRVNQICGTTSISSFQSLTAVIW
RCITRARRLPLDRETSCRVAADNRGRMYPPLHKDYFGNCLSALRTAAKAGELLENDLG
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/product="CHP-rich zinc finger protein-like"
/protein_id="BAB09185.1"
/db_xref="E158572"
/translation="M5LYFEGHEHHVSIIKHRDGLECDACDRSFGDVISCGECKFTVH
/translation="M5LYFEGHEHHVSIIKHRDGLECDACDRSFGDVISCGECKFTVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /LTANSlation-"MDSSSSVKIVSKSFVKPKTLPEESKOPYYLSPWDYAMLSVQYIQ
KGLLFHKPPLDSIDTLLEKLKDSLAVTLVHFYPLAGRLSSLTTEKPKSYSVFVDCNDS
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RCAIREPTPVALSNMKVHEHTLTLMPRLISFVCDACGMKGDRAPYVCVQCDFMIFHQE
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GLGKGVTLRSGYAHKFDGKVSAYPGREGGGSIDLEVCLVPEFMEALESDEEFMSLVSL
Submitted (24-OCT-1997) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
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/product="N-hydroxycinnamoyl/benzoyltransferase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subun1t"
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/product="US snRNP auxiliary factor, small a
join(5306. .5761,5932. .6828)
/note="gene_id:MBD2.2"
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compLement(1. 218)
/note="CDS is reported in Acc# AB007647
gene_id:MJB21.20"
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/db_xref="GI:9758571"
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ETEWTNEKHÄLVLKSMEASFVDQLYNSLGALGKNENVSESTRFGSGRKPSQEQFKVLH
DGFWQKINYKQPEHRINGRHGGNSHEFLRSPWIKHYRPLYKTOIPVTDEPENOVVSS
NGKKGICSSSASSLKQLSSHSRDHDQISVGEEVSDQNFVNEGIKGENGSSKRMKTVM
MSESSSTDQESVGTBEREKETDQESVAIEHLQKQ"
complement(30319. .31245)
                                                                                                                                                                                                                                                                                                                                          /translation="manTQLKSDAIMDMMKEHLSTDAGKEVTEKIGLVYQINIAPKKL
GFEEVTYIVDLKKGEVTKGKYEGGKVDATFSFKDDDFVKVATGKMNPQMAFIRGAMKI
      PEGRNKENGFGQSKSFAFGEQGSSSNNTGGSTTTNNNLTPETKKKKKKKLSLFPKVFM
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27989. .23171,28527. .28634))
/note="gene_id:MBD2.9
pir |T05226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MVGDYRGRFSSRRFSDDSDDSSDDASSVEGETTSSMYSAGKEYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence~not_experimental
/product-'non-LTR retroelement reverse transcriptase-like
                                                               .23461,24198. .24300,24565. .24625
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0; Mismatches 458; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to unknown protein"
                                                                                                                                                                                         similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
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/db_xref="GI:9758578"
                                                                                                                                                                                                                                               /evidence-not_experimental
/protein_id="BAB09190.1"
/db_xref="G1:9758577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 135.2;
                                                        complement(join(23380.
24707. .21832),
/note="gene_id:MBD2.8
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/codon_start=1
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Best Local Similarity 48.5%;
Matches 439; Conservative
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                                                                                                                                                                                                                                                                                                     QSWCPDCVRAEPVIYKTLEEFPEEVKLIRAYAGDRPTWRTPAHPWRYDSRFKLTGVPT
LVRWGCDSVKGRLEDHQAHLPHLILPLLARST"
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COMplement(join(10994. .11250,11343. .11490))
//note="gene_id"xBD2.4
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTDMITMNATLRMLYRNTGTFFGVHVTSSPIDLSFSGITIGSGSIKKFYGSRKSGRTV
VVNVLGDKIPLKGSGSTLVPPPPAAPIPKPKKKRGPTVIEPPAAPPAPVPMRLNFTVR
SARYUGKLVOPKFYKRIVCLINFEHKKLSKHIPTINNCTVTSI"
complement(10in)114641. 14694,14770. 14868,15144. 15272,
15358. 15401,15497. 15569,15650. 15736,15848. 15932,
16050. 16123,16204. 16733,16863. 17553,17677. 18603))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVEGSSEMLVDSDSILETPLVASPTLRFLDEKEQDFRESTNVEDYCEEDGSSGVVVEN
CLEASSWPSETYSEGSGNVEIFVERFREALAEDAYGSSDLOSKQELTAPPESVEIAT
LGSADQADMGSIGTSGGGSSTGSPVQDENKTITKDMHISAGDFEKSOSAGSESILQPE
IEEEOFSFSDLDECKPGGNSSVGSSSDTVKVDGKESYDETKTSPEKGVENTMALSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INIERKKDIFTDEMERLVGSLPIMRLQNNDDMDASPSQPLSQSFDPCFNTSKLDLRED
ESSSGGLDAESVAESSPKLKAFKHVIANPEVVELSLCKHLLSEGMGAEAASQAFNSEK
LDMEKFASLGPSILENDKLVVKIGGCYFPWDAAAPIILGVVSFGTAQVFEPKGMIAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNEKPGDVLAGGSGSWKLWPFSLRRSTKEAEASPSGDTAEPEEKÖEKSSPRPWKKTVR
ALTPFSEQLASLDLKDGMNSYTFTSTNIYGTQQVDARIYLWKWNSRIYVSDVDGTIT
RSDVLGQFMPLVGIDWSQTVTHLFSTNIKOLIFLSARAISQASVTRQFLVNLKO
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RDTDEISYLKVGIPRGKIFIINPKGEVANNRRIDTRSYTNLHTLVNRMFPATSSSEPE
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DELRWAKELSEQAKRGMSTIESRLVEAKKEMEAARASEKLALAAIKALOETESSORFE
EINNSPRSIIISVEEYYELSKOALESEEEANTRLSEIVSOIEVAKEEESRILEKLEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MHAKTDSEVTSLSASSPTRSPRRPAYFVQSPSRDSHDGEKTATS
FHSTPVLTSPMGSPPHSHSSSSRFSKINGSKRKGHAGEKQFAMIEEEGLLDDGDREQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MNAVGRIGSYIYRGVGTVSGPFHPFGGAIDIIVVEQPDGTFKSS
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VYTSGGDRAFTTSRDDVVDKVFIPLKSGRONYDSPSPRTGNCKIVGRPGILCYVFGG
RSVRESQDCGVERAEIAADLLEVKWSTNIDTRKRGKGMSSESLDGKDYGESTFGSKS
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RAFVYPRSVESPRFGSPRSVESPCFGSPIGVIDTASPFESVREAVSKFGGITDMKAHK
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IEMVSNEYKDMLREKELAAERADIAVLEAKEIERTMDGLSIELIATKELLESVHTAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTELAAFTDISSGNLLLEKNDIHAAVESARRELEEVKANIEKAASEVKKLKIIAGSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NREMSVRKAELKEANGKAEKARDGKLGMEQELRKWRSENGKRRTDEGREPEKSPTRSS
                                                                                                                                                                                                                                                                              /translation-"MTLKKVDANPSTLESSLQELKSDETSRSKINFILFLADNDPTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MLGDDKDSDDLNLFLNAIGEAGDEEGPTSFNDIDFLTFDDEDLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>EAEEKRFSVAMARDQDVYNWEKELKMVENDIERLNQEVRAADDVKAKLETASALQHDL</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>IQTIERRKMVDEELEKIQEAMPEYKREAELAEEAKYDALEELENTKGLIEELKLELEK</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPRRCYVLAFIVGFSLLFAFFSLILYAAAKPQKPKISVKSITFEQLKVQAGQDAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strong similarity to unknown protein"
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/note="gene_id:MBD2.7
                                                                                                                                                                                                                                                                                                                                                                                                                               gene_id:MBD2.5
similar to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"gb|AAF23287.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFNTWNFWKLPPPSLM"
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ATTSTSGVVrbndsarkkytndovyrtrendckykrasnlog*StebqlasrbslukgeI
ATGSYRSSGRDHKQYEPRKSRRTHSNRESTTGLSSEMGNSAGSLFRDKETQKRAGEIH
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STRTSRIPFREFDEDSRKERHIPSPSKRFREFSRGRLSNRFSLKDISAGOPLSSSEDTI
MSGSMRFDGSVCFSQSNPFNGYTHCRSRVSPLRFFLDPLLKFRASESVLPSKRRSSS
SNPKPITNSNVPLQDEKKQDASRTLAIFQLTIRNGIPLFQFVVDDNSSSSRSILGATM
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FPEKGAPSPLISRWRSGGLCDCGGWDVGCKLHVLSNKTVLHKFNQSFTLFDQEVSEQD
SSPALAMTELKTGIYRVEFGSFVSPLQAFFVCVTVLTCASKAKTTGKSSSPMAPPLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                VKVLNKEGLOGHREWLTEVNFLGQLRHPNLVKLIGYCCEDDHRLLVYEFMLRGSLENH
LFRSNPRTLLHFLKMMIALGAAKGLAFLHNAERPVIYRDFKTSNILLDSDYTAKLSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLAKAGPQGDETHVSTRVMGTYGYAAPEYVMTGHLTARSDVYSFGVVLLEMLTGRKSV
ARTRESKEØUIVDWARRKLNDKRKLLQIIDPRLENQYSVRAAQKACSLAYYCLSQNPK
ARPLMSDVVETLEPLQCTGDALIPCATTTAGAAFAMGGVPDYRMHRRFAKNVGFGAIC
RSPNNYSPGGPAACRVR"
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                                                                                                                                                                                                                                                              protein kinase NAK, Arabidopsis thaliana, EMBL: AL162874"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity to predicted proteins, Arabidopsis thaliana"
                                                                                                                                                                                                                                   /note="strong similarity to serine/threonine-specific
                                                               complement(Toin(1726. .2207,2629. .2752,2857. .2962,3091. .3556,3633. .3687))
/gene="F7J8_5"
/gene="F7J8_5"
3091. .3556,9633. .3687))
/gene="F7J8_5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(6055. .8082,8214. .8420)
/gene="F738_10"
/note="EST F14175 marks 5' end of this gene; 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2208. .2628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2856)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contains an intron
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/gene="F7J8_10"
6055. .8082
/gene="F7J8_10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2963.
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/gene="F7J8_5"
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1726. .3687
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1 (bases 3758 to 118507)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (26-JUL-2000) MIPS, at the Max-Planck-Institut fuer
Submitted (26-JUL-2000) MIPS, at the Max-Planck-Institut fuer
Submitted (26-JUL-2000) MIPS, at the Max-Planck-Institut fuer
Buchcement, Am Klopferspitz 18a, D-82152 Martinsried, FR6. E-mail:
lemcke@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
E-mail: michael. bevan@bbsrc.ac.uk
On Jul 27, 2000 this sequence version replaced gi:6759425.
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.
Location/Qualifiers
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                                                                            6444 AAAAGCTGGTGAACTATTGGAGAATGATCTTGGATTTGCTGCTTTGAAAGTGCATCAAGC 6503
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Arabidopsis thaliana DNA chromosome 5, BAC clone F7J8 (ESSA
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                                                                                                                                GATCGTGAAGCATGACGCTAAGGCCATTGATGAAAGAAACAAGGAGTGGGAGAGCAACCC
                                                                                                                                                                               2 (bases 1 to 3766)
Bevan, M., Rose, M., Hempel, S., Entian, K.-D., Bancroft, I., Mewes, H.W., Rudd, S., Lemcke, K. and Mayer, K.F.X.
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EU Arabidopsis sequencing, project.
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complement(1726. .2207)
/gene="F7J8_5"
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EQMIPTONGSIDGPT INVEGOTILY WITHWIGVEQLKSVWMDGANMIT
QCPIQPSNNFTYQFDITGQEGTLLWHAHVVNLRATHGALITRPRSGRPYPPRYKE
VPLIRQQWMYYDVRLLELRPAPYSDAYLINGLAGDSYPCSKNBYFNLKVVQGKTYLLR
IINAALMTHLERIANNYTVVQAVYTTPYLTDWAILTFGGTIDAILTAAQPIGTY
YMAILPYFSAIGVPRASDYRFPRGLIVYEGATSSSSPTKPWMPPANDIPTAHRESSNI
TSLVGGPHRYDDEKMTTWGLGLIDPQPSNAKVVGPANDANMANNT
                                                                                                                                                                NSTVETVLQUITGILTPESHPMILLIGFNEYVLGYGFGNYDPIRDARKLALENPQMHNTV
GVPFGGWYVLRFIANNPGIMLFHCHMDAHLPLGIMMAFIVQNGPTRETSLPSPPSNLP
GCTRDPFIXISRTTNVDMSY*
complement(13626..13810)
/gene="F7.18_30"
                                                                                                                                                  RISMQEAYFYNITGVYTDDFPDQPPLKFDFTKFEQHPTNSDMEMMFPERKTSVKTIRF
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
/translation="MPRVHHSLSNQAFLVLLLFSSIASAAIVEHVLHVKDVVVTPLCK
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Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81127 TGTTTCCTCTCGGAAATCCAGATGGAGCTTCGATCACGATGGGGGAGCTCGCCGAGATTCC 81186
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AB005249.1 GI:2264321
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                                                                                                                                                                                                                                                                                                                                                                                             860 TCTCCACATTCCAATCACTCTCCGCACACGTGTGGCTAGCCGTCACACGTGCGCGCCCAAC 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  920 TCAAGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGTTGATC
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                                                                                                                                                                                                                                                                                           Score 131.8; DB 13; Length 118507;
Pred. No. 1.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1340 TGGAGATTAGTTTGGAAGCANATGCTATGGAGAGGTTGGAGAAAGATAAAGAGTT 1394
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52.9%;
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Arabidopsis thaliana
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Matches 283; Conservative
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EQIIPAANGSLPGPTINVREGDTLVVNVINNSTYNVTIHWHGVFQLKSVWMDGANKIT
EQIIPAANGSLPGPTINVREGDTLCVHVNVINNSTYNVTIHWHGVFQLKSVWMDGANKIT
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VPITFQQWWTDYYLGLRPAYSDAYLINGLAGDS PCSENRWFNLKVVQGTYLLR
IVNAALNTHLFFRIANHNVTVVAVDAYSTPYLTDVMILTPGQTVDALLTADQAIGKY
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SLVGGPHWTPVPRHVDEKMFITMGLGLDPCPAGTKCIGPLGQRYAGSLNNRTFMIPER
ISMQEAYFYNISGIYTDDFPNQPPLKFDYTKFEQRTNNDMKMMFPERKTSVKKIRFNS
TVEVLQNITAIISPESHPMLHGFNFYVLGYGFGNYDPIRDARKLNLFNPQMHNTVGV
PPGGWWYLRFTANNGCWLFHCHMDAHLPYGIMSAFIVQNGPTPETSLESPPSNLPQC
TRDPTIYDSRTTNIDLSY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(13626. .13810,13898. .14866,14987. .15097,
15387. .15631,15775. .15926,16131. .16229))
/gene="F7J8_30"
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15387. .15531,15775. .15926,16131. .16229))
/gene="F7J8_30"
13626. .16229
                                                                                                                                         complement(join(8811. .8995,9120. .10082,10181. .10291,
10608. .10852,10996. .11147,11461. .11559))
/gene="F7J8_20"
/gene="F7J8_20"
                                                                                                                                                                                                                                                           complement(join(8811. .8995,9120. .10082,10181. .10291,
10608. .10852,10996. .11147,11461. .11559))
/gene="F7J8_20"
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                                                                                                                                                                                                                                                                                                                                /note="strong similarity to lacil0 laccase, Populus trichocarpa, EMBL:PTY13773"
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/number=1
                                                                                         .8995)
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/gene="F7J8_20"
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/number=3
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/gene="F7J8_10"
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                                                                    'number=2
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81126

1279

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AACITSLSKNLLWFADISSSVAEDNKIDTLQLTEKKLEEHETNLRLNSSDNIAAVSSI
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Institute, Department of Plant Gene Research; 1532-3, Yana, Kasaracu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3934)

Address for correspondence: Raos@kazusa.or.jp

Rof the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MXM12

Genes with similarity to proteins in the databases are described in protein similarity to proteins in the databases are described in protein similarity to proteins in the databases are described in protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gow/Grail-1.3/), GENSCAN (Chis Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of SplicePredictor (Volker Brendel. Stanford University, http://gremlini.cool.iastate.edu/cgi-bin/sp.cgi).

Genes encoding tRNAs are predicted by tRNAscan-SE (Seen Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE).

This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
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join(7023. 2363.2483. 2573,2733. .2804,2904. .3005,

1016(7023. .2363.2483. .3366,3503. .3553,3630. .3711.3915. .4009,

4090. .4161,4233. .4349,4501. .4569,4679. .4736,4833. .4954)

/note="contralis similarity to unknown protein

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QEVVKVPRVESKLRVFSFKIQFGTQITKLTKGLNAVNSACEEIRTSQKLKDIMENILC
LGNILNQGTGRGRAVGFRLDSLLILSETRADNSKMTLMHYLCKVLASKASDLLDFHKD
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TQVATVMALYYPARGNAEALAHYFGYHYPFEQVTATLLSFIRLFKKAHEENVKQAELE
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TFSFLYSDYLLQVYREALRHTWLVHESVFESQICELHRLYRRQKELMMEMBEFRHNKA
LYLNSGCFPPRTHWMSSSISAYQTRUPHEEDNISRLLVDNKVGKFFEKKKYLDLELPP
FEYSDMLEEVHEAQURLEEQSLQRMSLDSGRQSKLOLDLNBPAKIEBHSDYYFNQFL
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VKKFETEKPQESSSVSLHGKHGLDQPQGVVQELPCLISTLLLDKRYKSLMTRSRSRNK
VKHCPSNKTFKGSDHDPHSSGQASSESQSNQTSMEKGSSSSLSEAKSAKKGTSLGNKR
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/note="gb|AAF67766.1
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similar to unknown protein"
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/protein_id="BAB09942.1"
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physically assigned Pl clones
DNA Res. 4 (3), 215-230 (1997)
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Nakamura, Y.
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                             DNA Res.
97471969
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                                                                                         REFERENCE
AUTHORS
                                                                                                                                                        TITLE
JOURNAL
                             JOURNAL
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VHING THE DESIGNATION OF THE STANDARD OF THE STANDARD STA REKFSGKVMEEIFDAVVVATGHYSHPRLPSIKGMDSWKRKQIHSHVYRVPDPFRNEVV VVVGNSMSGQDISMELVBVAKEVHLSAKTLDISSGLSKVISKHPNLLIHPQIESLEDD GKVIFVDGSWVVADTILYCTGYSYKPPFLESKGRIEVDDDRVGPLFBHTPPPCLSPSL STKOIPPKLIGFPFFBAQAKWIAQVLSGKSSLPSPDQMLQSVDEFYRSRDLAGVPKHN THDIAADFTYCDKYADVVGFPHLEDWRKLLCLSALNNSQENLETYRDSWDDHELLQEAL OSSHFTNFNS" /LTGTSIGLIGOTONESSENISQUDECCLDDANPMEISVETIPVVDEEVQGDDDVLHP
AAETNHASILKRYSTRYLDKKTGKAQVQTRYRGNQTSSTHDLCKHGKRREEDLVIKPWK
VAKKNVDSSCDLGKGETLRKSLGNVSFPDKSSLGAAKREAAGEVVKSCDGLHVKRSET
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LEKTDLEVKTGT
LEKTD NKNSKEERLKNLKNKEKTNIDEPVRPDDAVEKTLYVVESSVEKKKKMSTKSVKISET QQSSEKKIIRSTGKKSLSLLPSLPPPSEVVTGSDPRPIRQTTSRSKTSLPEKKQSGSA NLVTNPKPESKIRPKRIGLKVTPPPPPTKQQMNFKKGKVLEPKPEDSTTTSIKFKKIV /translation="MVTFTSEASRSRSKKVCVICAGPAGLVSARELRKEGHKVVVLEQ NEDVGGQWFYQPNVEEEDPLGRSSGSINGELKVHSSIYSSLRLTSPREIMGYSDFPFL /translation="mevSEEQRRRDEATRLAFAEKRRQSFDSSENPQRQQDFRLAKCR KLDGSNDVCPQEGYRNYEPVRVLSTSVPEKFRVRLEICSPDSFSVTPVQLQGFRCPEE LAVVEKLSOSYISGKWOPCLPEHYTEEKVEQLIETLPRKLVNALLPFQLDGLRFGIRR GGRCFIADEMGLGKTLQAIAIAGCFISEGSILVVCPAVLRFTWAEELERWLPSCLPSD KRLRPLPLEKRRTY INKAAPELFARKNLLETLVNDPTBGNÄWHADH I IPVYQGGGECR LENMRTLCVACHADVTAAQCAERK LI RSKARKQLKNTLNELRNNPKQKDLSADENTKE **AKKGRDMRRFPGHKELWLYLKDFSEAFGLREMIRFNVRVEFVGEKEEEDDVKKWIVRS** QECLRQLRKILSDAIPLHYTQNDDGGRAGVYKIRDYNKVSGCLKRSKSVEVEGVPWKT SKSSPPKPVDAFTSSGEEKTGVDWGALRKRRGSRIPAADFKHMIINQVV°
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10412 . 10494,10570 . 10728,10817 . 10887,10981 . 11557))
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complement(21177. .22862)
/note="gene_id:MXM12.6
unknown protein"

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Arabidopsis thaliana
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DBC-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.blochem.mpg.de_rnayer@mips.blochem.mpg de Project Coordinator: Mike Sevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
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Bevan, M., Van Der Schueren, J., Chuang, Y.J., Voet, M., Robben, J., Volckeart, G., Bancroft, I., Mewes, H.W., Lemcke, K. and Mayer, K.F.X. Unpublished
                                                                                                                                                             32314 CTTATGATCATGAAATTCGTTGTAGCCTTGCCGCTAACAATGGAACAAAATTGGATCCAC 32373
                                                                                                                                                                                                                                                                        32494 TTGGAAACACTAGTGAAGTGGTCTCGGAGACAATCAAAAACTGGTTGAAATCATCTTATG 32553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAATAGGTTTGATGGAATGGTGTATTTGTACCAAGGCAAAAATGGAGGAAGAAGCATTG 1336
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Arabidopsis thaliana DNA chromosome 5, BAC clone F13G24 (ESSA
                                          CAATGCCAGAAAGTTACTTJGGCAACCTAATTCAGGCAATTTTCACAGTGACCG---CGG
                                                                                     3234 CATTGTCTTTGAGCTATCTTGGTAATTGTCTTTCTGCTGTAAAGTCCAAGACCGTTACAT
                                                                                                                                     CAGGTTTGTTACTAGCAAGCCCGATCGAGTTCGCTGGTGGGATGATACAACAAGCGATCG
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EU Arabidopsis sequencing, project.
Direct Submission
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/db_xref="taxon:3702"
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AL133421
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KEYWORDS
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                                                                                     /evidence-not_experimental
//potedn_id="BAB0947.1"
//db_xxef="G1:0176717"
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EVYTODQCNIKTPCREPCMRMSGLFGFSKGCLHMKRWDELNSFLTATAAVUTFGLNALR
GRHKLRGKAMGGAWDHINTQDFLNYTVSKGYVIDSWEFGNELSGSGVGASVSAELYGK
                                                                                                                                                                                                                                            DLIVLKDVINKYYKNSWLHKPILVAPGGFYEQOWYTKLLEISGPSVVDVYTHITYLG
SGNDPALVKTIMPESYLSQVSKTFKDVNQTIQEHGPWASPWVGESGGAYNGGRHVSD
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KGVLAVQTDGPPOLIVKYAHCSKGRACYTLLINLSNQSDFTVSVSNGINVVLNAESRK
KKSLLDTLKRPFSWIGSKGRACYTLLINLSNQSDFTVSVSNGINVVLNAESRK
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COMPLEMENT (29080. 29607)
//note="gene_id; kXmi2.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence-not_experimental
//potesin_id="BAB09948.1"
//db_xref="G1:10176718"
//translation="MLQEQPVALSFRPNSFRRSMETGVDRDDRGWTQLHIKAREGDL
KAYKELLDGQADVNALACGPKSKGWTPLHLAAKGGHIEVMDLLLERGANMEARTSGAC
GWTPLHAAAKERKRENVFLVGNGAFLPDDITDSRFNPPVQYCHGLEWAYEERKKLSE
DTSLSCGDTSCSSAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MDSTSSEVKIVSQCFVKPKTIPEKWKEPYHLSPLDLVMLSMHYL
QNGLLFLKSDDATKTKDFMETWLQKLRDSLAETLVHFYPLAGRLSTLKTDNPRSYSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32093 AGGGTACGGT---CCTGTGTACAACCTTCCTTTCACTCACTCACTCATGAATTCATTAGCCG 32149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCTTTTCAAGCGTTAGCCGCATTTATGTGGAGATGCATTACAAGAGCAAGAACTTAC 32313
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/product="anthranilate
hydroxycinnamoyl/benzoyltransferase-like protein"
/protein_id="pak80949.1"
/db_xref="GI:10176719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567 TGTGCTGGATGGTACTTCGACGTGGCACTTTATGACCTCGTGGTCCGAGCTTTGCTGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32033 ACAAGAAACCGATAACTTGCTTCTCAAGAATCCTCCAGTCCTTTCACGTTGGTTTCCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 83599;
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                   /note="contains similarity to heparanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(31233. .31706,31923. .32819)
/note="gene_id:MXM12.9"
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                                          gene_1d:MXM12.7"
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11145. .13478
/gene="113G24.30"
john(11145. .11303.11400. .11436,11532. .11715,11814. .11962,
12037. .12273,12372. .12561,12665. .12790,12901. .13000,
13095. .13478)
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LEKTDLEVRKVSRISENKASKEDTLEKNKEKALIDEPVRCDDVLEKTSLDAQVVSRISE
OKSSEKLIRENLKNKSKELDEPVRPDDAEKTLIVVSSSVEKKKMSTKSTSE
OKSSEKLIRSTGKKSLLIPDEPVRPDDAEKTLIVTOVESSVEKKKMSTKSTSTST
OKSSEKLIRSTGKKSLLIPDEPVRPDDAFKLOVATSRSKTSLIPEKKOSGSA
VOEBKLATSDVNKKKSLLKNTPPPPPTRQOMTSKKOKVLRHEKVETTSIKKKIV
BETVNKLEEVRKSKVKALVGAFETVISLODNNTTSOKKKIOTTENNVI
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/protein_id="CAB62597"
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LFGFSKGCLHMKRWDELNSFLTATGAVVTFGLNALRGRHKLRGKAWGGAWDHINTQDF
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LVAPGGFYEQQWYTKLLEISGPSVVDVYTHHIYNLGSGNDPALVKKIMDPSYLSQVSK
TKDVNQTIGEHGPWASPWYGESGGAYNSGGRHVSDFIDSWYLDQLGMSARHNTKV
YCROTLYGGFYGLEKGTYNDNDDYSALLWHRLMGKGVLAVOTDGFPPQLEYARHCSK
GRAGYTLLLINLSNGSDFTVSVSNGINVVLNARSRKKKSLLDTLKRPFSWIGSRASDG
YLNNEEYHLTPENGVLRSKTWVLNGKSLKPTATGDIPSLEPVLRSVNSPLNVLPLSMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"MSEENISQVDDRCCLDDANPMEISVETIPVVDEEVQGDDDVLHP
AAETNHASLKRYSTRVLDKKTGKAQVQTRYRGNQTSSTHDLCKHGKRREEDLVIKPWK
VAKKKNVDSGDLGKGETLRKSLGNVSKPDKSSLQAAKREAAGEVVKSCDGLHVKKSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(5773. .7458)
/note="similarity to mature parasite-infected erythrocyte
surface antigen, Plasmodium falciparum, EMBL:AF056936"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative protein"
/protein_id="CAB62594.1"
/db_xref="GI:6562296"
                                                                                                                                                                                                                                                 .4523)
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5773. 7458
/gene="F13G24.20"
complement(5773...7
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/gene="F13G24.30"
/number=1
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/gene="F13G24.30"
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/gene="F13G24.30"
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/number=15
   complement (3628.
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/gene="F13G24.30"
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                                                                                                                                             complement(join(<445. .585,727. .888,1047. .1145,1228. .1293, 1410. .1520,1618. .1719,1847. .2046,2155. .2220,2394. .2565, 2965, 3025,3257. .3347,3554. .3627,3851. .4026,4311. .4443,4524. .4883,5052. .5396))
April and a complement of the compleme
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MEVSEEQRRRDEATRLAFAEKRKQSFDSSENPQRQQDFRLAKCR
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                                                                                                                                                                                                                                                                                                                                                                        /product="putative protein (fragment)"
/protein_id="CAB62593.1"
/db_xref="G1:6562295"
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/number=12
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/number=2
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                                445. .5396
/gene="F13G24.10"
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/number=4
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/number=11
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complement(1521.
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/number=10
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/chromosome="5"
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prediction programs including GRAIL (ftp://arthur.epm.orni.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Mashington), Genscan (Chris Burge, Mittp://gnomic.staniford.edu/GENSCANW.html), and NetplantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST admanual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin, X., Kaul, S., Reunsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D., Fujli, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feidli, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Reidli, C.Y., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Moffat, K.S., Cronnin, L.A., Shen, M., VanAken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:2088638. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
17149 TTTTCCATTTAGAAAAACTTTTGGGAGCGATGGTGGTTCACATTGGAAGCTCTCCGAGGT 17208
                                                                                                          TTAAGATGTATGAATGCGAGTTTGGGATGGGAAAAGCGGTTGCGGTTAGAAGCGGTTATG 17268
                                                                                                                                                                                                                     17269 GCGGTAAGTTTGATGGGAAGATATCAGCATATGCAGGAAGAAGAAGGAGGAGGAACCATAG 17328
                                                                                                                                                                                                                                                                                                                                ATTIGGAAGTATGTCTTCTAGAGTTTATGGAAGCTTTGGAATCAGATCAAGAATTCA 17388
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATGGAAACTGCTTAATTTGCTTAGCTTGGACTCAACTGGCTACACTTTATTATGAGC 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence and analysis of chromosome 2 of the plant Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thallana chromosome II section 215 of 255 of the complete sequence. Sequence from clones T517, T28M21, F27II. AF002109 AE002093
AF002109.2 GI:6598791
                                                      TCAAGGTTTACGACGTGGATTTTTGGATGGGGAAAGCCAGAGAGTGTGAGGAGTGGTTCGA
                                                                                                                                                                 ACAATAGGTTTGATGGAATGG'IGTATTTGTACCAAGGCAAAAATGGAGGAAGAAGCATTG
                                                                                                                                                                                                                                                                            ATGTGGAGATTAGTTTGGAAGCAAATGCTATGGAGAGGGTTGGAGAAAGATAAAGAGTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16969 CATTGTCTTTGAGCTATCTTGGTAATTGTCTTTCTGCTGTAAAGTCCAAGACCGTTACAT 17028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17029 CCGGTGAGCTACTAGAAATGATTTGGGATGGGCTGCTTTGAAAATGCATGAAGCTGTGA 17088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGGAAACACTAGTGAAGTGGTCTCGGAGACAATCAAAAACTGGTTGAAATCATCTTATG 17148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16568 TGTGGGAGATGGAGGTTCCTTGTGGCATTTTTTCAACTCTTTGTCGGAGATTTTCAATGC 16627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16628 ACAAGAAACCGATAACTTGCTTCTCAAGAATCCTCCAGTCCTTTCACGTTGGTTTCCTAA 16687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16688 AGGGTACGGT---CCTGTGTACAACCTTCCTTTCACTCACTCGATGAATTCATTAGCCG 16744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATGCCAGAAAGTTACTTCGGCAACCTAATTCAGGCAATTTTCACAGTGACCG---CGG 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGTTTGTTACTAGCAAGCCCGATCGAGTTCGCTGGTGGGATGATACAACAAGCGATCG 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACATTCCAATCACTCTCCGCACACGTGTGGCTAGCCGTCACACGTGCGCGCCAACTCA 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 AGCTGTGCAGCTCACCAAGCTCAAGGACGGGCTCACCATGGGATTAGCATTTAACCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  743 ACGGTGATGTCCCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAAGTTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16849 CTTCTTTTCAAGCGTTAGCCGCATTTATGTGGAGATGCATTACAAGAGCAAGAACTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 923 AGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGGTTGATCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAAGCATGACGCTAAGGCCATTGATGAAAGAAACAAGGAGTGGGAGAGCAACCCGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTTCAGT - - - ACAAAGATGCTGGAGTGAACTGTGTTGCTGGTTGGAAGTTCGCCAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             683 GAGTCAAGCTCAACCTCTCAACCATCAGATGCACCCGAACATGCTAAGTCAGCAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      803 AGTTAGCAATTGACAAAATCAAGTCAACAGTCAATGCCAACTCAGGAGAGGCGCCATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            = = = = = =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 119.2; DB 13;
larity 49.2%; Pred. No. 1.3e-17;
Conservative 0; Mismatches 463;
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                            /number=3
11716. .11
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12372. .12
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                                                                                                             /number=3
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Matches 476;
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22037. .22139
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/rpt_family="(TA)n"
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29872. .29961,30172. .>30411)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(29280. 29414,29559. 29658,29750. 29787,29872. 29961,30172. 30411)
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MSNTEIVYQLYPSMVRRISNASPKEHLPQEEETGVLSDDKMDDEAKEPPREQNSKTGV
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HQDSTTLSSSSVLGSEFVDYEEHSSAELDKELISISNDLNNTAWIRSGKEAEQSLKAD
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GOPPAIKNLLFRIMARGGYIAVSTLISALLPFLGDFWSLTGAVSTFPLTFILANHMYY
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LAGFIYGRRAYHLTWGLQYVNLFMINCGFIILAGSALKAVYVLFRDDHTMKLPHFIAI
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/rpt_family="POLY_A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLQTTRSWDFMNLTLKAERNPENESDLVVAVIDSGIWPYSELFGSDSPPPPGWENKCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFTPLQKDKVSWAFLRALKNGTLTSAAAGNYANNGKFYTVANGAPWYWTVAASLKDR
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DEQKKGKLWDYYKKDQSKERLAKIHKTEEIPREEGWVPTVAHLSSRGPNCDSFLANIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAIAFHTFLLQLLLFFRASFAEANDSRKTYLVQMKVGGHRYGSS
SGHQELLGBVLDDDSYKESFTGFSASLTPRERQKLMSKTTTVSSRRRENGEVSRSRNL
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GLALYLKSFKRWSPSAIKSALMTTSSEMTDDDNEFAYGSGHLNATKVRDPGLVYETHY
QDYIDYLCKLGYNTEKLRSHVGSDKIDCSKTEIDHDADLNYPTMTARVPLPLDTPFKK
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RNWNKNRAEMTRNTWLTWTEKDGSRQVRSPIVIYSIKGPKACM"
Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by LRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.
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/protein_id="AAB95271.2"
/db_xref="G1:6598792"
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/note-"Sequence from clone T28M21"
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/organism="Arabidopsis thaliana"
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/gene="At2g39860"
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/gene="At2g39860"
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Location/Qualiflers
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/chromosome="II"
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QLSNYSSMEGVVYCRPHFEQLFKESGSFSKNFQSPAKPLTDKPTPELNRTPSRLAGMF
SGTQDKCATCTKTVYPIEKVTVESQCYHKSCFKCSHGGCPISPSNYAALEGILYCKHH
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Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-AUG-2000) Takuji Sasaki, National Institute of Aproblological Resources, Rice Genome Research Program: Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakieabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
                                                                                                                                                                                                                                        59140 TCTCGTCGTTTCAATCTCTATGCGCGTTGCTTTGGCGTGCGATCACACGTGCGAGGAGG 59081
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Oryza sativa genomic DNA, chromosome 6, BAC clone:OSJNBa0075G19,
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:OSJNBa0075G19
                                                                                                                                                                   Indels
/product="putative LIM-domain protein"
/protein_id="AAB95275.1"
/db_xref="G1:2088643"
                                                                                                                                              Pred. No. 1.7e-14;
0; Mismatches 268;
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                                                                                                                             Score 106.2;
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Matches 267; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTCGCGAAAGAGTATTCAAGTTCTCCGAGTTAGC-AATTGACAAAATCAAGTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85894 CACTTCTCATCGGAGTCGCTGGTGGCGCTCAAGGAGCGGGCTCGCCAAGAGCTCCTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              832 GTCAATGCCAACTCAGGAGAGAGCCCATTCTCCACATTCCAATCACTCTCCGCACACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              892 TGGCTAGCCGTCACACGTGCGCGCCAACTCAAGCCCGAGGACTACACTGTGTAACACTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 102.8; DB 13; Length 88318;
Pred. No. 1e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 522;
Tel:81-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from
clone.
                                                                                                                                                                                                                                                                       /clone="OSJNBa0075G19"
a 19394 c 19436 g 24509
                                                                                                                   1. .88318
/organism="Oryza sativa
                                                                                                                                                                            /cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="6"
                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.1%;
Matches 455; Conservative
                                                                                                                                                                                                                                                                                                        24979
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us-08-894-356c-3.rge

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source
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
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ATF11C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNRS, Avenue de la terrasse, 91198 Gif sur Yvette Cedex, FRANCE (Location/Qualifiers
                                                                                                                                                                                                                                                                                                   Medicago truncatula
Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I;
Fabales, Fabaceae, Papillonoideae, Medicago.
              1138
AAGCCAGAGAGTGTGAGGAGTGGTTCGAACAATAGGTTTGATGGAATGGTGTATTTGTAC 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   959 ATTGCAGGAAAAGGGTTGATCCTCCAATGCCAGAAAGTTACTTCGGCAACCTAATTCAGG 1018
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                                                                                                                                                                                                                 02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="sequence flanking the T-DNA right border in transgenic line Sy5" $727\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ATTGTCGTCACAGATTAAACCCAAAAATGGAACCGTTTTATTTCGGTAACGCAATACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1309 CAAGGCAAAAATGGAGGAAGAAGCATTGATGTGGAGATTAGTTTGGAAGCAAATGCTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 94.4; DB 14; Length 2072; 50.0%; Pred. No. 6.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                              Medicago truncatula genomic DNA, Sy5 (RB) locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (28-MAR-2001) Ratet P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3880"
/note="Sy5 (RB) locus"
                                                                                                                               1369 GAGAGGTTGGAGAAGATAAAGAGTT 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /variety="R108"
                                                                                                                                                                                                                                                         AJ310831.1 GI:13539595
                                                                                                                                                                                                               2072 bp
                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 2072)
Scholte, M.
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hes 236;
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Matches
                                                                                                                                                                                                                              DEFINITION
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1249
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VERSION
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TITLE
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                                                                                                                                           85294
                                                                                                                                                                                     RESULT 10
MTR310831
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AUTHORS
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DPNLHGLPEVTRPNQDQNVQNHKQSHSESGKEVVEERPEETTGDSWVISIRDKLEQAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDDDTTIWGKICITYVVHYLOENDKKSYFPOTVSLGPYHHGKRELRPWERHKWRALNK
KLRKRKORIEBSTRANARELEERRARACYGEPIGISRNEFTERALULDGCYVELERGTVE
GFTELGYARNDPVFARGLMHSIORDMIMENOLPLFVLDRLLELOLGTONGTVAH
VAVKFFDDLMPTGEALTKPDGSKLMNMLEKSLDTLGDKGELHCLDVFRRSLLOGSPPT
WYRSLLKRITRVDTRYDGVYFRQQQLVHYTELRRAGVRFRRKRTDFWDIEFEFKNGYLEIP
KLLIHDGTKGLFSNTTAFEGOTHIESSNHTSYSIIFWDNINGISEDSYLHYGGIIEHP
KLLIHDGTKGLFSNTLAFEGOTHIESSNHTSYSIIFWDNILINGSEDSYLHYGGIIEHP
IGSDSEVADLFNRLCQEVVFDPRGSHLTSKSCDVNRYVNRKMNVLKATLTHKYFNNPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-APR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemckedmips, blochem.mpg.de,mayerdmips.blochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue Gaston Cremieux, BP191, 91006 Evry Cedex, France;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F1161_10"
complement(join(2238. .2668,2807. .3330,3449. .4119))
/note="similarity to various predicted genes, Arabidopsis
thaliana and Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.cns.fr
On Apr 20, 2000 this sequence version replaced gi:6434207.
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 105654; 110423 to 111122)
Bargues,M., Collado,M.C., Navarro,P., Terol,J., Perez-Alonso,M.,
Mewes,H.W., Rudd,S., Lemcke,K., Mayer,K.F.X., Quetier,F. and
1259 GTGTGAGGAGTGGTTCGAACAATAGGTTTGATGAAGGAATGGTGTATTTGTACCAAGGCAAAA 1318
                                                                           321 CTATAAGGAGTGGTAAAAAGTAATAAATTTGATGGTAAAATTTCAGCTTTTCCTGGTAGAG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATF11C1 111122 bp DNA PLN 19-APR-2000 Arabidopsis thaliana DNA chromosome 3, BAC clone F11C1.
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                                                                                                                                                           ATGGAGGAAGAAGCATTGATGTGGAGATTAGTTTGGAAGCAAATGCTATGGAGGTTGG
                                                                                                                                                                                                     AGAAAGATAAAGAGTTCCTCATGGAAACTGCTTAATTTGCTTAGCTTGGACT 1430
                                                                                                                                                                                                                                                                                                                                                                                                 441 AAAATGATGTGGAATTTATGCAGTATGTTACGGATGTAGTGTGTGAAAT 492
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/variety="Columbia"
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2238. .4119
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LAGSPYEFEGKMAGDPFWYMRLIGYPAQVTNLFRSSAYNDMFCVELTLTMVIKFNPFV
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TNFDAVVEPLDICKGKYPGGRGGQVFKRAVYGEHLVSKVQTNFAM"
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/db_xref="G1:652301"
/db_xref="G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14718. 16609
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15266. 15312,15360. 15461,15544. 15660,15743. 15804,
15899. 15935,16035. 16098,16167. 16285,16375. 16490,
16576. 16609))
/note="similarity to SRG1 protein, Arabidopsis thallana,
PIR:S44261"
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                                                                                  complement(join(12843. .12868,13035. .13704))
/note="similarity to predicted protein, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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Pred. No. 1.3e-05;
0; Mismatches 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(14859. .14984)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .15265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(12843. .12868)
                           12843. .13704
/gene="F11C1_40"
complement(join(12843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(14985.
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Matches 402; Conservative
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RVADKHLQRV PTVTELRDAGFKFKLNKTDRFWDIKFSNGYLEIPGLLIHDGTKSLFL
NLIAFEQCHIESSNDITSYIIFWDNLIDSPEDISYLHHCGIIEHSLGSNSEVADMFNQ
LCQEVVFDYRDIYGIYTIFWDRCYKQNYSRKLNSLKTTLILKYLDNFWAYLSFFAAV
ILLILFSQSYPAAYAYFNPSS"
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GSMHSIRRDMLMLENQLPLMPTYMPSTKIENSQENNIK FFHBIADKDK EELHCLDVFR
RSVLQPSLKPEPRLSRNSWRWPVADRYRQKLLHCYTELREAGIKFKRRK SDRLMDIG
FKNGCLEIPKLLHDGTKSLLSPNLAKFEQCHIDSTKQITSY IIFVENLINSNEDYRYL
OYCGIIEHWLESDSEVVDLFHKLCQDVVFDPIDSYLYPLCLGVDRFYSLILLLLTFCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative protein"
/protein_id="CAB62297.1"
/db_xref="CI:6523029"
/db_xref="CI:6523029"
/translation="METF07PPPPPPPPPPPLPRGRAPPPOPPPPPPPPRL
GPRLARLLPPPRQQLARLRKQQPLVLPEPLPRRSPHATPWLTGHDVKKGKSYDKLREY
VENVRRQNEESERVVLPKSISYEDQNLENGQDTRSKPGINEVVEGSGTKRLEWVISIK
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KWRAVNWVLKRTNQGIEVFLDAMIELEEKARACYEGSIVLSSNEFTEMLLLDGCFILE
LLQGVNEGFLKLGYDHNDPVFAVRGSMHSIQRDMIMLENQLPLFVLNRLLELQPGTQN
                                                                                                                                                                                                                                                                                                                         5324. .7543
/gene="Filc1_20"
complement(join(5324. .5760,6099. .6562,6678. .7543))
/note="similarity to various predicted genes, Arabidopsis thaliana and Oryza sativa"
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/note="similarity to various predicted proteins,
Arabidopsis thaliana and Oryza sativa"
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10931. .11550))
AYFSFSAAVILLLTLCOSFYAVYAYYKPNSKL"
complement(2238 .2668)
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/protein_ld="CAB62298.1"
/db_xref="GI:6523030"
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complement(10931. .11550)
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/number=1
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/number=2
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/gene="F11C1_30"
complement(9545. .9615)
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                                   36687 TTGAAGTACTTCCTTTCCCGCCGATTTCAAGAGCTGTGATGGTGTCTCGTTGCCTTG 36746
                                                                                                                         36867 ACAGGITCATGITICAATIACAAGCCICTIGITCICAAAGGGIGGITCCTIGAGGGGAIC 36926
                                                                                                                                                                                                                                36927 GATTACCCAATCCATGTTCCAGTTTCAGAGGCAGAGGTCACCACCAAGCCGTGAACCT 36986
                                                                                                                                                                                                                                                                                36987 TCTTCCGTGCCCATTACGAAAGAATGGATTTTTCACTTCACAAAGAAGAATATTTCAGAT 37046
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                                                                                                                                                           TIGCAGGACTIGATICCTIGIAATAAAAICTIGAATTIGGAAGGGCTICATCGCCCTCTT
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                                                                                                                                                                                                                                                        745 GGTGATGTCCCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAAGTTCTCCGAG
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DNA US 5670367

 166494
 7218 bp

 Sequence 14 from patent

 166494

 166494.1

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DEFINITION ACCESSION VERSION

KEYWORDS

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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis,
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Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1530-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Kisarazu, Chiba 292-0814, 1438-52-934)
Address for correspondence: koos@kazusa.or.jp
Por the latest information on annotation of this clone, please see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H. and Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB020742 74342 bp DNA PLN 27-DEC-2000 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K21H1 AB020742 BA000015 GI:3985931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1224 TTACGACGTGGATTTTGGATGGGGAAAGCCAGAGGTGTGAGGAGTGGTTCGAACAATAG 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1284 GTTTGATGGAATGGTGTATTTGTACCAAGGCAAAAATGGAGGAAGAAGAAGCATTGATGTGGA 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1044 TTTGTTACTAGCAAGCCCGATCGAGTTCGCTGGTGGGATGATACAACAAGCGATCGTGAA 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1104 GCATGACGCTAAGGCCATTGATGAAAGAAACAAGGAGTGGGAGAGCAACCCGAAGATCTT 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1164 TCAGTACAAAGATGCTGGAGTGAACTGTGTTGCTGTTGGAAGTTCGCCAAGGTTCAAGGT
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                                               1 (bases 1 to 7218)
Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                                                                                                                                                       /organism="unknown"
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DNA Res. 7 (1), 31-63 (2000)
20181125
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/clone_lib-"Mitsui TAC"
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DWCSDFDITWFELPNIGNIHGGFMKALGLQNNCSWPKEPLSNPDRKSPLAYYSIRDSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETEEHSFRHRWLI FVSLVLLKLLRFFSKLLALVGSALEFSLNFLSNNSFSGLFLRGEV
VMPQRTSENYQSFIGHLDTRVSLDMTLNREDGEKYYAALSIMASKIAYENAARIKHVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGEFMEKKLEKYNIKYYRFVYNNDIVPRLPYDDKDLMFKHFGTCIYYDQNYQAKVMRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTPQDYKNSRVVSINGYEDVPRKDETALKRVIFIPTG"
7772. .8497
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
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similar to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="gene_id:K21H1.4"
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/note="emb|CAB62312.1
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FINASSECTION TRANSPARATION AND TRANSPARATION TO THE TRANSPARATION TRANSP /evidence**not_experimental
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FSTITISPITISTREKTIYATTDSVORESAVLTNESELQARKHRGYVSFTKDLPVKHT
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FNSSSLCNKKLIGAKVFNKGLFANNPDLRETKIGQYSSPYDTIGHGTHVAAIAAGNHV KRKIMOPCWIKI ISSEGTCSPSEGNENCKEUTYQSPKINTILVSEEKYVHPPATYTAI
MKTIYUNEGNISETYSASVLCFHNAKIDVPMPAPERKRSGILSHFYVRNPEGTGYP
IGWKEVSDENSKNGCNVLSIENSERALLNRLFLELNKLDSDILVGHNISGPLDVLL
ORAQACKYQESHWSKTGRLKREFMPKLKGNSYKGGAPPGLMSCIAGRLLCDPDLCSR
DLLKEVSYSITDLSKTQLNRPRKEIAPNDIRKHQSSKTLVELIECGETDAMLSMELM
FHLSVLPLTTQLTNISGNLWGKTLQGRAQATERYKTLHFKKFILDRFISGNETH
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LLLDFNSLYFSIIQEYNICFTTIPRSEDGVPRLPSSQTPGILPKLMEHLVSIRKSVKL ASLANEKSVÜDNLGDDCNEIVRCFGEDRTVENGEEMHNLFLEYASRGSLESYLKKLAG EGVPESTVRŘHTGSVLRGLRHIHANGFAHCDLKLGNILLFGDGAVKIADFGLAKRIGD LTALNYGVQ RGTPLYMAPESVNDNEYGSEGDVWALGCVVVEMFSGKTAMSLKEGSNF PESTDESDDGGRFSGRLKKKKGKGROTQOPQVKKVNPALKAAATITGEGRLSSMFTSS SKKVKETDEXQYPGTILDAUTPDESDRKKHTRRKLGGTVPYTIFKKKLESYAS SMGKRESEPTPSTY EGDSVSMDNELMKEDMKESEVIPSETMELLGSDIVKDGSNKI RKTEVKSELGVKEVFTLNATIDMKEKDSALSATAGWKEAMGKVGTENGALLGSSSEGK TEFDLDADGŠLRFFILDAYEBAFGASMGTIYLFGKVKMGDTYKSCCVVVKNIQRCVYA IPNDSIFPSHELIMLEQEVKDSRLSPESFRGKLHEMASKLKNEIAQELLQLNVSNFSM APVKRNYAFERPDVPAGEQYVLKINYSFKDRPLPEDLKGESFSALLGSHTSALEHFIL MSLLLRIGYGDEVPMIPEELSEQGRDFLSKCFVKDPKKRWTAEMLLNHPFVTVDVDHD VLVKEEDFVVNMKTEDVSTSPRCPFEFPDWVSVSSGSQTIDSPDERVASLVTDMIPDW KMKK ETGLKYWELDIRQQALKLTANSMYGCLGFSNSRFYAKPLAELITLGGRDILQRT VDLVQNHLNLEVIYGDTDSIMIHSGLDDIEEVKAIKSKVIQEVNKKYRCLKIDCDGIY KRMLLLRKKKYAAVKLQFKDGKPCEDIERKGVDMVRRDMSLLSKEIGDLCLSKILYGG RQRGYKEGFNAKDTVPY11CYEQGNASSASSAGIAERARHPDEVKSEGSRWLVDIDYY LAQQIHPVVSRLCAEIQGTSPERLAECLGLDPSKYRSKSNDATSSDPSTSLLFATSDE /db_xref="G1:10177595" /translation="MEWIRGETIGYGTFSTVSLATRSNNDSGEFPPLMAVKSADSYGA SCEDVVEATHNELMKIKEEMRNGQVALEKYVITKTLTKPPAAYPDSKSQPHVQVALRM ESKKPATPETEESDSTFWLKLHCPKCQQEDSTGIISPAMIANQVKRQIDGFVSMYYKG IMVCEDESCKHTTRSPNFRLLGERERGTVCPNYPNCNGTLLRKYTEADLYKQLSYFCH ILDTQCSLEKMDVGVRIQVEKAMTKIRPAVKSAAAITRSSRDRCAYGWMQLTDIVI complement(join(26828. 27019,27114. 27179,27258. 27323. /note="emb|CAB16798..27834))
gene_id:K7!": gene_id:K21H1.7 similar to unknown protein" /evidence=not_experimental /product='DNA polymerase a complement(15607. 17817) /note="gene_id:K21H1.5" complement(join(26828. 27414. .27485,27598. .2 /codon_start=1 SVTNSWVTVR

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NEEETLERYWRNWLOSSTNGOSETGSQEEYTNASSHGGTFIYEEETLEGYRRNWLOSS
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KKRRSKINEKMKALQKLIPNSNKTDKASMLDEAIEYLKQLQLQVQTLAVMNGLGLNPM
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                                                                                                                                          RLPQVPPPTHTRINETLEQDLNLETLLAAPHSLEPAKTSGGMCFSTATLL"
complement (101n(29326. 29986, 29960. 30082,30390. 30512,
30845. 30958,31036. 31233))
/note="gene_id:K21H1.8"
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/note="contains similarity to MAP3K-like protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37732 AATGGGCTTGGTTGGGCTGCATTGCAAATAAACAAAACTGTTGGGTCACAAACGAATGAA 37673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37555 TTCGGTTGGGGTAAACCAATAGCGGTTCGAGCTGGACCGGGAAATACCACCGATGGTAAA 37496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 305; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67; DB 12;
Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                    similar to unknown protein"
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Best Local Similarity
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RESULT

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Assaki, T., Matsumoto, T. and Yamamoto, K.

Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

Submitted (19-FBE-2001) Takiji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondal
2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasakiedar-affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.

* NoTE: This is a "working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Coation/Qualifiers
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Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae;
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   'G 21-FEB-2001
*** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                    1 (sites)
Saski, ". Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone: P0529E05
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Oryza sativa (cultivar:Nipponbare) DNA, clone:P0529E05
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         HTG
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                                clone P0529E05,
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0; Mismatches 282;
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                                Oryza sativa chromosome 1 clone
PROGRESS ***, in ordered pieces
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137205 bp
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Matches 256; Conserv
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918 -ACTCAAGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGTTG 976
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Cryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:B1096Al0
L bublished Only in DataBase (2001) In press
2 (bases 1 to 151703)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (A8-MAR-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* This sequence will be replaced
* by the finished sequence will be preserved.
* the accession number will be preserved.
* the accession number will be preserved.
* the accession number will be preserved.
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Oryza sativa (cultivar:Nipponbare) DNA, clone:B1096A10.
Oryza sativa
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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                  1217 T---CAAGGTTTACGACGTGGATTTTGGATGGGGAAAGCCAGAGAGTGTGAGGAGTGTT 1273
19133 TCCCCATGTATGAGGGCAACGACTTCGGGTGGGGCCCCCCTCGCGGTGGGGACGGCC 19074
                                                                                                                                                  19073 GCGCCAACAAGTTCGATGCCAAGATGTCGCGGTTCCCTGCCCGGGGGCGGGGCGCGGG 19014
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a 36328 c 37093 g 38853 t
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
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VERSION
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us-08-894-356c-2.rst

, Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. TITLE Generation of ESTs from tomato fruit tissue JOURNAL Unpublished (1999) COMMENT Contact: David Frisch Clemson University Genomics Institute	Tol: 864 656 436 Tal: 864 656 436 Fax: 864 656 4203 Email: dfrisch@cLEMSON.EDU 5 prime sequence. FEATURES Location/Qualifiers Location/Qualifiers Source //Olone="CiEF783" //Clone="Lip="fruit pericarp" //Lissue_Lip="fruit pericarp" //db_note="Yope" "fruit pericarp" //db_note="Source" //db	DASE COUNT 142 a 140 c 117 g 184 t ORIGIN Ouery Match Best Local Similarity 56.4%; Score 152; DB 113; Length 583; Best Local Similarity 56.4%; Pred. No. 1.3e-27; Matches 325; Conservative 0; Mismatches 245; Indels 6; Gaps 2; Oy 58 CAAGTTCTTGGAAATGCCCACCCGCGCGCCGCCGCGCGCG	0y 235 GTCCCTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGGTCGGT 294 19 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 535 CAATCTTCATCATCTTGSTGATGCCAGTTCTTTTTTAATAAATTATGGGT 594
SUMMARIES Result Query No. Score Match Length DB ID Description	152 9.4 583 113 AW2210S0 150.6 9.3 690 155 BG59947 150.6 8.9 570 142 BB922784 140.6 8.7 76 142 BB922784 133.4 76 159 167 BE8434257 125.2 7.7 497 122 AW616206 119.2 7.6 487 118 AW616208 119.2 7.6 487 118 AW650280 119.2 7.6 487 118 AW650280 114.6 7.1 564 142 BB921494 114.6 7.1 564 142 BB921494 112.4 6.9 508 173 BG097054 108.8 6.7 574 142 BB922746 108.8 6.1 788 164 BB187619 89.4 5.5 687 111 AW102336 89.4 5.5 687 111 AW102336 89.8 6.1 788 164 BB287619 89.4 5.5 687 111 AW102336 89.4 8.9 549 21 AL490445	4.6 578 197 197 197 197 197 197 197 197 197 197	56.4 3.5 311 166 BE353747 BE353747 55.8 3.4 307 142 BE920010 BE920010 55.8 3.4 307 142 BE920010 BE920010 55.8 3.4 49 138 BE660848 BE660848 54.2 3.3 648 154 BC457806 BG457806 AM21050 583 bp mRNA TION EST297519 tomato fruit mature green, TAMU Lycopersicon esculentum N AM221050 583 pp mRNA sequence. AM21050 101:6532734 DS EST. LOMA CLONG CLEF3F3, mRNA Sequence. AM21050 101:6532734 DS EST. LOMA CLONG CLEF3F3, mRNA Sequence. AM21050 101:6532734 DS EST. LOMA CLONG CLEF3F3, mRNA Sequence. AM21050 101:6532734 DS EST.	Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae: euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon. REFERENCE 1 (bases 1 to 583) AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.

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AW221049
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

E 1 (bases 1 to 690)

S van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,

Bougri, O., Buell, C. R., Ronning, C., Tanksley, S. and Baker, B.

Generations of Esrs from sprouting potato eyes

L (Dnpublished (2000)

Tontact: Cathy Ronning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries

Dlysland to the contact Research Genetics, Libraries

Dlysland to the contact Research Genetics, Libraries

Dlysland to the contact Research Genetics, Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anote—"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI: Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers: The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
'
                                                                                                  BG599447 690 bp mRNA EST 12-APR-2001
EST504342 cSTS Solanum tuberosum cDNA clone cSTS25122 5' sequence,
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS25122"
546 TCTACTCCACAAATTACGTGGACATGAACCAATCTT 581
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l (bases 1 to 606)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,W.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST297518 tomato fruit mature green, TAMU Lycopersicon esculentum cDNA clone cLEF3F1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Skol; cEEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seeds and locules were discarded prior to freezing the
TTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTATTACCACTTTT 486
                                                     359 CTTTGTTCCTACGTTAGGGGAACCTAAGGATGCACCGGGGTCCAATTAGCTCCGGTCTT 418
                                                                                                              TGCTTTACAGGTGACGGTGTTCTCCAACACCGGTATATGCATTGGACGCAATCTTCATCA 546
                                                                                                                                              547 AGTICITGGIGAIGCCAGITCITTICIGCATTITAAIAAATTAIGGGITTIGGTIGACAA 606
                                                                                                                                                                                                                                                                                        479 TGTTGTTGGTGGAGCTACCATAGTAGGTTCATTAGGGCGTGGGCTCTACTCCATAA 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1999
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/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
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/cultivar="TA496"
/db xref="taxon:4081"
/clone="cLEF3F1"
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Pred. No. 2.9e-27;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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Contact: David Frisch
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( ( ) Dases 1 to 570)

Van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hanssen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBlueScript SK(-); Site_1: EcoRl; Site_2:
Xhol; Tissue was supplied by Dr. Fry (Cornell University).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE922784 570 bp mRNA EST 02-OCT-2000
EST426553 potato leaves and petioles Solanum tuberosum cDNA clone
CSTB22E2 5' sequence, mRNA sequence.
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Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdnafresgen.com.
                                                                                                                                                                                                                                                                                                                       425
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                                                                                                       129 TTACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAAAACATTATTCCTCCTCTTAAAAA 188
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 CCCACTGTCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTT 177
                         CTACAGATTCCGCCATCCTTGTCCCAACTC - - TAAATTTATCATTCATCCATTAAATC
                                                                                                                                                                                                                                                                                                 355 AATTGCAGAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTA
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                                                                                                                                                                                                                       295 AGATTCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAAC
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/tissue_type='leaflets and petioles"
/dow_stage="8 weeks old plants"
/lab_host="SOLR"

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    /organism="Solanum tuberosum"
    /cultivar="Kennebec"

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/clone="cSTB22E2"
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AUTHORS
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COMMENT
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EST499600 P. infestans-challenged leaf Solanum tuberosum cDNA clone BPLI10A14 5' sequence, mRNA sequence.
BG591758.1 GI:1360998
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(bases 1 to 763)
Zhang, P., Hernandez.M., Tornqvist, C.-E, Wirtz, U., Loukolanov, A., Rangel, P., Haberlach, G.T., Cho, J., Chlemingo, A., Bougri, O., Buell, C.R., Ronning, C.M., Helgeson, J. and Baker, B.
Generation of ESTS from Potato Leaves Challenged with Phytophthora incompatible Reaction
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Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized greely. The tissue was immediately frozen liquid nitrogen. 115 g 180 t
                                                                                                                                                                                                                                                                                                                                                                              TTGAGAAATGCCGTGTTGCGCCACCACCGGACGCCGTCGCCGAGTTTACAGTCCCACTGT 125
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He Institute for Ganomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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                                                                                                                                                                                                                                                      Query Match 8.9%; Score 144.6; DB 142; Lengt
Best Local Similarity 57.0%; Pred. No. 9.2e-26;
Matches 305; Conservative 0; Mismatches 224; Indels
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Solanum tuberosum
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                                                                                                                                                                                   /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Whole plants were challenged with 450,000 sporangia/ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTCAACTGACCACTTTTTCCGAATCTTGGTGTATCCATTGGTTTCAACCATCATGTT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 GCCGTGTTGCGCCACCACCGGACGCCGTC-GCCGAGTTTACAGTCCCACTGTCGTTTTTC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 GACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTTCTACAGATTCGGCCAT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGATATTATTCTACAAGCTCCCCATT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 CCTTGTCCCAA---CTCTAAATTTATCATTCATCCATTAAATCGTCCCTTTCCCTTGTT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 TCCAAACCCGATTTCGTTCAAAACTTTATTCCTACTCTTAAAAATTCACTCTCCCTCACT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 CTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTAGATTCCTCCGATAGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 ATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGAGC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 ATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTATAAATTCAACGATTTG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 ATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTATTACCACTTTTTGCT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 GTTCCTAAGTTAGGGGAACCTAAGGATGCACCCGGGGTCCAATTAGCTCCGGTCTTAGCC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491 TTACAGGTGACGGTGTTCTCCAACACCGGTATATGCATTGGACGCAATCTTCATCAAGTT 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551 CITGGTGATGCCAGTTCTTTTCTGCATTTTAATAAATTATGGGTTTTGGTTGACAAATCC 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 155; Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 140.6; DB 155; Length
Pred. No. 9.8e-25;
0; Mismatches 259; Indels
                                                              /cultivar="kennebec"
/db_xref="taxon:4113"
/clone="BbLi10A14"
/clone="lb="P. Infestans-challenged leaf"
/tissue_type="leaf"
/dev_stage="6 week old"
                                                    /organism="Solanum tuberosum"
               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  156 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.78;
56.38;
Seq primer: M13F-R
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Best Local Similarity 56.3
Matches 346; Conservative
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/note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first stgn of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp." 129 c 121 g 182 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                l (bases 1 to 591)
Johan, Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
                                                                                                                                                                                 Lycopersicon esculentum
Sukaryota, Vitidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
                      EST405335 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 TGTGACAGGAGATTCTGTGTCTCTTATTTTCGAGACTGATATGAATTATCT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAAATTTATCATTTCATCCATTAAATCGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 GTTAGCCGGGAATTTGATTTGGCCGGTAGATTCCTCCGATAGAATGCCGGAGTTGCGTTA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 CAAGAAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGAGCATGGATTTTGATTATCT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCCGGAGATCATCAGAGGGATTCTTATAAATTCAACGATTTGATTCCGCAGCTGCCAGA 447
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24-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation of ESTs from tomato fruit tissue, breaker stage
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Pred. No. 6e-23;
0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruit, TIGR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4081"
/clone="cLEG15H6"
/clone_lib="tomato breaker fr/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon/cultivar="TA496"
                                               clone cLEG15H6, mRNA sequence.
  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: dfrisch@CLEMSON.EDU
                                                                          BE434257
BE434257.1 GI:9432100
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56.6%;
591 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prime sequence.
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Location/Qualifiers
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                                                                                                    262
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VERSION
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van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
'F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tankaley, S.D.
Generation of ESTs from wild tomato (Lycopersicon hirsutum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lýcopersicon hirsutum
kararyota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="L. hirsutum trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded
mixture of cells which is highly enriched for trichome
likely with minor contaminations of other types of leaf
                                                                                                                                                                                                                                                                                                                  EST 24-MAR-2000
EST307245 L, hirsutum trichome, Cornell University Lycopersicon
hirsutum cDNA clone cLHT1D15 5', mRNA sequence.
AW616206
AW616206
G:7322240
                                                                                                414 TATAGCAGGGTTCATTAAGGCGTGGGCTCTACTCCACAAATTCGGTGGACAT---GAACA 470
                                                                                                                                  628 GTTCCTTCCACTTTCTTCTCTACCTATGTACGACAGATCTGTGGTGCAAGATCCATTTCA 687
                                                                                                                                                      568 TITICIGCATITIAATAAATTATGGTTTTGGTTGACAAATCCAATGGAGATTCATTAAA 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 GTTGATCTCTGATGCAGAACACCATCTGCATTTCTACAGATTCCGCCATCCTTGTCCCAA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 TCCGAATCTTGGTGTATCCATTGGTTTCACTAACCATCATGTTGTTGGTGATGGAGCTAC
CTCCAACACCGGTATATGCATTGGACGCAATCTTCATCAAGTTCTTGGTGATGCCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 118; Length 487;
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.es 199; Indels
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Corganism="Lycopersicon hirsutum"
/db.xref="taxon:62890"
/clone="cLHT1D15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
111 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: David Frisch
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.9%; Score 128.6; Best Local Similarity 57.2%; Pred. No. 9.4e Matches 274; Conservative 0; Mismatches
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                                                                                                                                                                                                      688 TATTCGTCGAAAATCTACAATGAAAGAAA 718
                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon.
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KEYWORDS
SOURCE
ORGANISM
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'Yourcalain', Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato fruit tissue (Generation of ESTs from tomato fruit tissue contact: David Frisch (1999)

Contact: David Frisch (1999)

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Clemson University Genomics SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW930934 497 bp mRNA EST 30-MAX-2000 EST356777 tomato fruit mature green, TAMU Lycopersicon esculentum CDNA clone cLEF42M23 5', mRNA sequence.
AW930934 GI:8106335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLEF - Fruit were tagged at the lom stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
382 TTATCTCGCCGGAGATCATCAGAGGGATTCTTATAAATTCAACGATTTGATTCCGCAGCT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AGGGGAACCTAAGGATGCACCCGGGTCCAATTAGCCCCGCTCTTAGCCATTCAAGTGAC 417
                                                                                                                                                                                                                                            TCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTAGATTCCTCCGATAGAATGCCGGGGTT 321
                                                                                                                                                                                                                                                                                                                                                                                       322 GCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGAGCATGGATTTTGA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 GCCAGAACCGATTGTAACCTCCGGCGACGAAGTATTACCACTTTTGCTTTACAGGTGAC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               502 GGTGTTCTCCAACACCGGTATATGCATTGGACGCAATCTTCATCAAGTTCTTGGTGATG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---CTCTAAATTTATCATTTCATCCATTAAATCGTCCCTTTCCCTTGTTCTCAAACACTT
                                                                                                                                                                                                                                                                                                                  181 TATGCCCTTAGCCGGAAACGTTGCTTGTCCACTAGATACAAACG---GATATCCTGAGTT
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/tissue_rype="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
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us-08-894-356c-2.rst

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Lycopersicon esculentum
                                                                                                                                                                                                                        Query Match 7.6%;
Best Local Similarity 56.4%;
Matches 273; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tomato.
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van der Hoeven, R.S., Garvin, D.F., Matern, A.L., Holt, I.E., Liang, F.,
Upton, J., Hansen, T.S., Ronning, C.M., Craven, M.B., Bowman, C.L.,
and Tanksley, S.D.
Generation of ESTs from tomato nutrient-deficient roots
Contact: David Frisch
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                              655
                                                                                                                                                                                                                         356 ATTGCAGAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTAT 415
                                                                                                                                                                                                                                            475
                                                                                                    236 TCCCTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTA 295
                                                                                                                                                                GATTCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACA 355
                                                                                                                                                                                Gaps
                                                                                                                     2 TCACTCTCCCTCACTCTCAAACACTATACGCCCTTAGCCGGAAACGTTGCTTGTCCACTA 61
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                                                                                                                                                                                                                                                                                                   476 TTACCACTTTTGCTTTACAGGTGACGGTGTTCTCCAACACCGGTATATGCATTGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                  AAATTCAACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTA
                                                                                                                                                                                                                                                                                                                                                                       239 GCCCCGCTCTTAGCCATTCAGGTGACACTTTTTCCGAATCTTGGTGTATCCATTGGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                     359 CTACTCCACAAATTCGGTGGACAT---GAACAATTCTTATCGAATGAGCTAATTCCATTT
                                                                       9
                                         Length 497;
                                         Score 125.2; DB 122; Lengt
Pred. No. 6.7e-21;
0; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA clone CLEW18020 5' sequence, mRNA sequêncê.
BF096979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
/cultivar="TA492"
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EST400516 tomato nutrient deficient roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        656 TACGACAGATCTGTGGTGCAAGATCCATTT 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF096979.1 GI:10902689
                                         7.7%;
58.0%;
                                                                       Matches 261; Conservative
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                                                       Local Similarity
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                                            Query Match
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JOURNAL
COMMENT
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BF096979
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SOURCE
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ORIGIN
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/note="Vector: pBluescriptSKmcUadapt; Site_1: 5' EcoRI; Site_2: 3' XhoI; Roots were harvested from plants grown under the following deficiencies/stresses: 10 mM Al, Zn, P, K, Fe,N. mRNA was isolated from indivdual treatments. Proportional aliquots of mRNA of each treatment were mixed and used for library construction."
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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1 (bases 1 to 518)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S, Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronnning,C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 GAATGCCGGAGTTGCGTTACAAGAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AATGCCGTGTTGCGCCACCACCACGGACGCCGTCGCCGAGTTAACAGTCCCACTGTCGTTTT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTTCTACAGATTCCGCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TTGACCATGTTTGGTTAGGGTTTCGCCGTATGAGGCGGATATTATTTACAAGCTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 ccarrcaggracacrrrrrccaarcrrggrarccarrggrrrcarraaccarcarg 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 CTCTCAAACACTATAGGCCCTTAGGCGGAAACGTTGCTTGTCCACTAGATACAAACG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGATICCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTATTACCACTITITG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 ATCCTTGTCCCAA---CTCTAAATTTATCATTCATCCATTAAATCGTCCCTTTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 GCATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTATAAATTCAACGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 482;
/clone="cLEW18020"
/clone_lib="tomato nutrient deficient roots"
/tissue_type="roots"
/dev_stage="5-6 weeks old"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 124; DB 144;
Pred. No. 1.3e-20;
0; Mismatches 205;
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Location/Qualifiers
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Matches 307; Conservative
                                                                                                                                                                                                                               Unpublished (2000)
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                                                                                           REFERENCE
                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                         COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                        /organism="Lycopersicon esculentum"
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/cultivar="TA496"
/dutivar="TA496"
/dutivar="TA496"
/clone="taxon:4081"

Nierman, W., Fraser, C.M., Giovannoni, J.J., Martin, G.B. and Tanksley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 TGTGACAGGAGATGCTGATTGTTTTTCGAGACTGATATGAATCTCAATTATCT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAATTTATCATTCATCCATTAAATCGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 rcaaaacarrarrccrcrcrraaaaarrcacrcraccrcrcaaacacraracccc 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 CTTAGCCGGAAACGTTGCCTGTCCACTAGATACAAACG---GATATCCTGAGTTACTTTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 GTTAGCCGGGAATTTGATTTGCCCGGTAGATTCCTCCGATAGAATGCCGGAGTTGCGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 CAAGAAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGAGCATGGATTTTGATTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 CGCCGGAGATCATCAGAGGGATTCTTATAAATTCAACGATTTGATTCCGCAGCTGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448 ACCGATTGTAACCTCCGGCGACGAAGTATTACCACTTTTTGCTTTACAGGTGACGGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 CTCCAACACCGGTATATGCATTGGACGCAATCTTCATCAAGTTCTTGGTGATGCCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 TCCGAATCTTGGTGTATCCATTGATTTCACTAACCATCATGTTGTTGGTGATGGAGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 119; Length 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173; Indels
                                                          Generation of ESTs from germinating tomato seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%; Score 119.2; DB 1
1larity 57.3%; Pred. No. 2.2e-19;
Conservative 0; Mismatches 173
                                                                                                                                                                 Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@cLEMSON.EDU
                                                                                                                                             Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .518
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                                                                                     Unpublished (2000)
Contact: David Frisch
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Solanum tuberosum
                                                                                                                                                                                                                                                                                                                    prime sequence.
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236; Conserv
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Matches
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                                                       TITLE
JOURNAL
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasteridas I; Solanales; Solanaceae; Solanum.

( (Dases 1 to 564)

( Dases 1 to 564)

( Chansen, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of ESTs from potato leaves and petioles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 CTACAAGCTACCAATTTCCAAACTCGATTTCGTTCAAACCATTATTCCTACTCTTAAACA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTGCAGAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AGTTCTTGAGAAATGCCGTG"TGCGCCACCACCGGACGCCGTCG---CCGAGTTTACAGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCACTGTCGTTTTTCGACATGCATGGTTGATCTCTGATGCAGAACACCATCTGCATTT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 CAATCTTCATCAAGTTCTTGGIGATGCCAGTTCTTTTCTGCATTTTAATAAATTATGGGT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475 ATTACCACTTTTTGCTTTACAGGTGTGTGTTCTCCAACACGGTATATGCATTGGACG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTGATTGAGCAATGCCAAG1TGCGCCACCTCCCCACGGCGCGCCAACAGAGCTAACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCCTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATTCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAAC
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                                                                                                                                                                                                                                                                                                            Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics,
Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 114.6; DB 142; Lengt
Pred. No. 3.1e-18;
0; Mismatches 234; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        petioles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="leaflets and petioles"
/dev_staga="8 weeks old plants"
/lab_host.*"SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4113"
/clone="csTB13B18"
/clone_lib="potato leaves and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism≔"Solanum tuberosum"
/cultivar≔"Kennebec"
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Mol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in limid attroom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B. Generation of ESTs from potato leaves and petioles (Unpublished (2000) Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 508)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG097054 508 bp mRNA EST 29-JAN-2001
EST461573 potato leaves and petioles Solanum tuberosum cDNA clone
CSTE45P9 5' sequence, mRNA sequence.
     382 TTTATTGAGACTGATATGAATTTCAATCGTTGGTAACCATCCTCGAAATGCTAAG 441
                                                                                                                                                                                                                                                                                                                              125 TCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTTCTACAGA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 GAGAAATGCCGTGTTGCGCCACCGGACGCCGTCG---CCGAGTTTACAGTCCCACTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GAGCAATGCCAAGTTGCGCCACCTCCCCACGGCGCAAACAACAAAAGCTCCCTCTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com. Location/Qualifiers
                                                                                                                                                                                                                                                                                               536 AATCT---TCATCAAGTTCTTGGTGATGCCAGTTCTTTTCTGCATTTAATTATGG
                                                                                  416 AAATTCAACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTA
                                                                                                                                      442 GATTTTTATCCCTTCATTCCTCAATTGGCACAACCTAAGGATGCACCGGGGGTCAAACTA
                                                                                                                                                                                       476 TTACCACTTTTGCTTTACAGGTGACGGTGTTCTCCCAACACCGGTATATGCATTGGACGC
                                                                                                                                                                                                                                              502 GICCCGGICTTAGCCATTCAAGTGACACTTTTTCCGAATCTTGGCATATCCCGTTGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.1e-17;
0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/tissue_ews_a weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .508 //
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db.xref="taxon:4113"
/clone="cSTB45P9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 t
                                                                                                                                                                                                                                                                                                                                                                                                     593 GTTTTGGTTGACAAATCCAATGGAGAT 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                      622 GGTTTACTCAACAATTCCGCGGTGAT 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 potato.
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
Asteridae: euasterids I; Solanales; Solanaceae: Solanum.

E 1 (bases 1 to 659)
S van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,
Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generations of ESTs from sprouting potato eyes
L Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1800-711-6195, email cdna@fresgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note—"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were trozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                  BG598154 659 bp mRNA EST 12-APR-2001
EST496832 cSTS Solanum tuberosum cDNA clone cSTS20M23 5' sequence,
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AGTTCTTGAGAAATGCCGTGTTGCGCCACCGGACGCCGTCG---CCGAGTTTACAGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 CCCACTGTCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 CCCTCTAACTTATTTTGATCTATATGGTTCGGTTTTGGCTATATGCGTCGGATTTTATTC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 CTACAGATTCCGCCATCCTTGTCCCAACTC - TAAATTTATCATTCATCCATTAAATCG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 TACAAGCTACCAATTTCCAAACTTGGTTCAAACCATTATTCCTACTGTTAAACAT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 TCCCTTTCCCTTGTTCTCAAACACTTTCCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 TCACTCTCCCTCACTCTCAAACACTACACCCTTAGCTGGCAACATTGCTTGTCCACTA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 GATTCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 AAT---TCGAGTGGTTATCCTGAGTTGCGTTATGTGACTGGAGATTCTATATCTGTTACT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 ATTGCAGAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTAT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%; Score 114.6; DB 155; Length 659;
55.0%; Pred. No. 3.2e-18;
tive 0; Mismatches 244; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Solanum tuberosum"
/cultivar="Kennebec"
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/clone_lib="cSTS"
                                                                                                                                                                                                                                                                                          BG598154.1 GI:13616294
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595 TTTGGTTGACAAA 607
                                ||| | ||||||
552 TTTACTCAACAAA 564
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Eukaryota; Viridian
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Sparmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 403)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning,
C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   potato leaves and petioles Solanum tuberosum cDNA clone
                                                                                                                                                                                                                           123 CTTAGCTGGCAACATTGCTTG%CCACTAAATTCGAGTGGTTAT---CCTGAGTTGCGTTA 179
                                                                                                                                                                                                                                                                                                               180 TGTGACTGGAGATTCTATATTCTGTTTTATTGAGACTGATATGAATTTCAATCATCT 239
                                                                                                                                                                                                                                                                                                                                                                         CGCCGGAGATCATCAGGGGATTCTTATAAATTCAACGATTTGATTCCGCAGCTGCCAGA 447
                                                                                                                                                                                                                                                                                                                                                                                                               240 CATTGGTAACCATCCTCGAAAGGCTAAGGATTT---TTATCCCATTCCTCAATTGGCACA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                            507
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                                                                                                                208 TAAATTTATCATTCATCCATSAAATCGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCC 267
                                                                                                                                                        268 GITAGCCGGGAATTTGATTTGCCCGGTAGATTCCTCCGATAGAATGCCGGAGTTGCGTTA 327
                                                                                                                                                                                                                                                                                    328 CAAGAAAGGGGACTCCGTTTC?TTAACAATTGCAGAATCGAGCATGGATTTTGATTATCT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 CTCCAACACCGGTATATGCAT/FGGACGCAATCTTCATCAAGTTCTTGGTGATGCCAGTTC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    568 TTTTCTGCATTTTAATAAATTÄTGGGTTTTGGTTGACAAATCCAATGGAGATTCATTAAA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 GTGCTTAGAGAATGAGTTCATTCCATTTTATGATAGGTCCGTGATAAAAGACCCTTATGA 533
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                        Length 574;
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Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                   0; Mismatches 222; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cultivar="Kennebec"
/db_xref="taxon:4113"
/colone="cSTB34B1"
/clone=lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
                        DB 142;
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                                                 Pred. No. 9e-17
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                          Score 108.8;
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     688 TATTCGTCGAAAATCTACAATGAAAGAAAAC 719
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                        6.78;
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                                                                   Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 574)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Llang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning Generation of ESTs from potato leaves and petioles
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE922746 574 bp mRNA EST 02-OCT-2000 EST426515 potato leaves and petioles Solanum tuberosum cDNA clone cSTB21L12 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Roning
Contact: Cathy Roning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                                                                                            481
                                                                                                                                                                                                                                                                                                                                                                                                                 359 TATCCCTTCATTCCTCAATTGGCACAACCTAAGGATGCACCGGGGGTCAAACTAGTCCCG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 GAATCGAGCATGGATTTTGATTATCTCGCGGAGATCATCAGAGGGATTCTTATAAATTC 421
ACTTATTTTGATCATATATGGTTCGGTTTTGGCTATATGCGTCGGATTTTATTCTACAAG 121
                                                                                                                                  TCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTAGATTCC 301
                                                                                                                                                        TCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATTGCA
                                                                                                                                                                                                                                                           TTCCGCCATCCTTGTCCCAA - - - CTCTAAATTTATCATTTTCATCCATTAAATCGTCCCTT
                                                                       122 CTACCAATTCCAAACTCGATTTCGTTCAAACCATTATTCCTACTCTTAAACATTCACTC
                                                                                                                                                                                                                                                                                                                                                                                           422 AACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTATTACCA
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/clone_lib="potato leaves and petioles"
/tissue_type='leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Solanum tuberosum"/cultivar="Kennebec"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 CATCAAGTTCTTGGTGATGCCAGTTC 567
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BE922746.1 GI:10448822
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE922746
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ORIGIN
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us-08-894-356c-2.rst

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/dev_stage="8 weeks old plants"
/lab_host="SOLR"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen.
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                                                                                                                                                                                                                                                                                                                                                           209 AAATTTATCATTCATCCATTAAATCGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCCG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 GCCGGAGATCATCAGGGGATTCTTATAAATTCAACGATTTGATTCCGCAGCTGCCAGAA 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 CC-----GATTGTAACCTCCGGCGACGAAGTATTACCACTTTTGCTTTACAGGTGACG 502
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                                                                                                                                                                                                                                                                                                                                                                                11 AAAACCATTATTCCTACTCTTAAACATTCACTCTCCCTCGCTCTCCAACACTATATGATT 70
                                                                                                                                                                                                                                                                  Query Match 6.4%; Score 103.6; DB 143; Length 403; Best Local Similarity 57.6%; Pred. No. 1.7e-15; Matches 228; Conservative 0; Mismatches 159; Indels 9;
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ORIGIN
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Search completed: November 5, 2001, 18:00:43 Job time: 14883 sec

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OFTANTION SISTEM: PC-10.2/MS-10.5

SOFTAMEE: PATENTIN RAIGASE #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/232,463

FILING DATE:
CLASSIFICATION JATA:
APPLICATION NUMBER: U$/07/935,313

FILING DATE:
APPLICATION NUMBER: EF 91 114 300.6

FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 1800 Diagonal Road, Suite 500
Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703)836-9300
TELERAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTR: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-232-463-14
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1819.738 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           November 5, 2001, 18:03:41; Search time 168.74 Seconds
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2: /cgn2_6/ptcdata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptcdata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptcdata/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptcdata/2/lna/pcTUS_COMB.seq:*
6: /cgn2_6/ptcdata/2/lna/pcTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-023-337-1

US-08-998-416-1137

US-08-998-416-288

US-08-998-416-186

US-08-998-416-186

US-08-954-659-11

US-09-103-429A-2

US-09-103-429A-2

US-09-103-429-90

US-08-906-768-90

US-08-906-768-90

US-08-906-768-90

US-08-102-411-90

US-08-611-90

US-08-611-90

US-08-611-90

US-08-05-14442A-90

US-08-06-611-90

US-08-06-611-90

US-08-06-113-90

US-08-06-113-90

US-08-06-113-90

US-08-06-113-90

US-08-06-113-90

US-08-06-113-90

US-08-06-113-90

US-08-06-113-90

US-08-764-100-13

US-08-764-100-13
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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č	₹*	2.5	961	9	5219739-16	Patent No. 5219739
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ค ั	9	2.2	099	Н	US-07-991-867B-32	33
'n	7	2.2	099	-	US-08-107-755A-32	32
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RESULT	1					
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; Sedı	lence 14, P	applicat	ion US.	/08	232463	
; Pate	Patent No. 5670367	0367				
; GE	GENERAL INFORMATION:	MATION:				
	APPLICANT:	DORNER, F.				
	APPLICANT:	SCHEIF	SCHEIFLINGER,	1		
	APPLICANT:	FALKNER,	R, F. G.	(1)		
. I	TITLE OF INVENTION:	IVENTION		OMB	RECOMBINANT FOWLPOX VIRUS	
	NUMBER OF SEQUENCES:	EQUENCE	٠.			
	CORRESPONDENCE ADDRESS	NCE ADD	RESS:			
	ADDRESSEE:	Fole	Folev & Lardner	rdne	£.	

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                                                                                                                                                                                                                                                                           185 ITCCGCCATCCTTGTCCCAACTCTAAATTTATCATTCATCCATTAAATCGTCCCTTTCC 244
                                                                                                                                                                                                                                                                                                                                                                   245 CTIGITCICAAACACTITCIICGITAGCCGGGAATITGAITIGGCCGGTAGAITCCICC 304
                                                                                          65 CTTGAGAAATGCCGTGTTGCGCCACCACCGGACGCCGTCGCCGAGTTTACAGTCCCACTG 124
                                               Gaps
                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Williamson, Valerie M.
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isgouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
  DB 1; Length 7218;
                                             88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
FILING DATE: 09-0C-1997
h 2.5%; Score 40.8; DB Similarity 2.5%; Pred. No. 0.091; 6; Conservative 146; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             023070-070210US
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APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08947823 Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: DNA (genomic) US-08-947-823-1
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nucleic acid
EDNESS: single
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California
       Query Match
Best Local Similarity
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US-08-947-823-1/C
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                                                    Matches
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                                                                                              1513 TTATGATGCAACAAATGTTTTAGGAGATTACAAATCCATGGGAAGATGTATCAAACTCAT 1572
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                                                                                                                                                 1472 TAAGAAAAAGTGGTATCAATGTATAAAAAGACAGACAAGTTATGATGCAACAAATGTT 1531
                                         Gaps
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Score 39.6; DB 3; Length 51952;
Pred. No. 0.57;
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                                       Indels
                                       :69
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                                       0; Mismatches
                                                                                                                                                                                                                                      32534 ATATTCCTTCAAAACATGTCAAAACAAA 32505
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CURKENT AFFLICATION NUMBER: US/08/463,975
FILING DATE: June 5, 1995
CLASSTETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12058
FILING DATE: L3 OCT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERRENCE/DOCKET NUMBER: 325800-331
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       1592 CAATTGTTTTAAAAAAAAAAAAAAAAAAAAA 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CARELLA, BYRNE, BAIN, GIL
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,97:
                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08463975; Patent No. 5618717; GENERAL INFORMATION:
APPLICANT: WEI, ET AL.
TITLE OF INVENTION: hABH
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.3%;
       2.48;
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       Query Match 2.4%
Best Local Similarity 54.0%
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEW JERSEY
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINEAR
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07068
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                                                                                                                                                                                                                                                                                                                                US-08-463-975-1
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APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Weller S. Thomas E.
TITLE OF INVENTION: AND PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
ADDRESSEE: Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1513 TTATGATGCAACAAATGTTTTAGGAGATTACAAATCCATGGGAAGATGTATCAAACTCAT 1572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,975
FILING DATE: June 5, 1995
APPLICATION NUMBER: PCT/US94/12058
FILING DATE: 21 OCT 1994
ATTORNEY/AGENT INFORMATION:
NAMME: FERRARG, GREGORY D.
REGISTRATION NUMBER: 36,134
                                                                          ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DCS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 325800-331
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1706
TELEFAX: 201-994-1744
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; Patent No. 5993827
; GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1953 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 59.1
Matches 65; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
                                    NEW JERSEY
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-09-023-327-1
                      ROSELAND
                                                                                                                                                                                                                                                               FILING DATE:
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                                                               COUNTRY:
STREET:
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59.1%; Pred. No. 0.29;
tive 0; Mismatches 45; Indels
                                                                                                                       GENERAL INFORMATION:
APPLICANT: WEI ET AL.
TITLE OF INVENTION: habh
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
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APPLICANT: WEI, ET AL.
TITLE OF INVENTON: habh
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEMART 6 OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: 1BM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,266

FILING DATE: 15-JAN-1997

CLASSIPICATION + 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,975

FILING DATE: JUNE 8, 1995

APPLICATION NUMBER: PCT/US94/12058

FILING DATE: 21 OCT 1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-023-327-1
; Sequence 1, Application US/09023327
; Patent No. 5929225
                                                                                   Sequence 1, Application US/08783266
Patent No. 5747312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET UNMBER: 32:
TELECOMMUNICATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ 1D NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1953 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.3
Best Local Similarity 59.1
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: CDNA
US-08-783-266-1
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1490 AATGTATAAAAAAGACAGACAAGTTATGATGCAACAAATGTTTTAGGAGATTACAAATCC 1549
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COMPUTER: TBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                   NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ. ID NO: 1137:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.3%; Score 37.6; DB 4;
Best Local Similarity 55.3%; Pred. No. 0.21;
Matches 73; Conservative 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Mendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 288, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
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APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 00
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                    SEQUENCE CHARACTÉRISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-08-998-416-288/C
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APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Mondland, Jurgen
APPLICANT: Mendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 0.97;
0; Mismatches 70; Indels
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                  CUSTON MAKE: TACHLIN KELEGER #1.0, VEISION CUSTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10.5EP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1593 AATTGTTTAAAAAAAAAAAAAAAAAAA 1622
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FILING DATE: 24-DEC-1997
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                        LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.39
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE:
US-08-487-826B-13
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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Length 636; Indels

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APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             Score 37.6; DB 4; Length 837;
Pred. No. 0.24;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                 PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-998-416-186/c
; Sequence 186, Application US/08998416
; Patent No. 6239264
; GENERL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Steiner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                            REFERENCE/DOCKET NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                  38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                 Query Match 2.3%;
Best Local Similarity 55.3%;
Matches 73; Conservative
ATTORNEY/AGENT INFORMATION:
               NAME: Melgs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
21P: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
                                                                                                                                                                                                                                                                        PAG1241RP
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US-08-998-416-288
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APPLICANT:
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1495 ATAAAAAAGACAGACAAGTTATGATGCAACAATGTTTTAGGAGATTACAAATCCATGGG 1554
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APPLICANT: Wingate, Vincent
APPLICANT: Wingate, Vincent
APPLICANT: Wolff, Mark
TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                         Length 615;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
COMPUTER: DATE: PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,659
                                                                                                                                                                                                                                                                                                                                         Score 37.4; DB 4;
Pred. No. 0.23;
0; Mismatches 56;
PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-554-659-11
; Sequence 11, Application US/08554659
; Patent No. 576761
               TELECOMMUNICATION INFORMATION:
TELEFAX: 919-541-869
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                    TOPOLOGY: Innear MOLECULE TYPE: DNA (genemic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
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Best Local Similarity 55.5%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 575 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       ORGANISM: PAG1074RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 11530-0299
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Query Match 2.3%;
Best Local Similarity 60.4%;
Matches 61; Conservative
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US-09-341-678-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                        1434 CGAATTTCATCAATAGTCTCCATGTGAGGAGCCCTTTGTAAGAAAAAGTGGTATCAATG 1493
                                                                                                                                                                                                                                                                                1494 TATAAAAAAGACAGACAAGTTATGATGCAACAAATGTTTTAGGAGATTACAAATCCATGG 1553
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Granados, Robert R
APPLICANT: Granados, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: cDNA and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                       ;
0
                                                                   Score 37; DB 1; Length 575;
Pred. No. 0.29;
0; Mismatches 95; Indels
                                                                                                     95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/103,429A
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Brown, Pinnisi & Michaels, P.C.
118 No. 6187558th Tioga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATORNEY AGENT INFORMATION:
NAME: MICHAELS, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTT-39
TELECOMUNICATION INFORMATION:
TELEPHONE: (607) 256-200
TELEFAX: (607) 256-368
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2821 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRGANISM: Trichoplusia ni
DEVELOPMENTAL STAGE: larva
TISSUE TYPE: peritrophic membrane
US-09-103-429A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09103429A; Patent No. 6187558; GENERAL INFORMATION:
DNA (genomic)
                                                                     2.38;
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                                                                                     Best Local Similarity 49.7
Matches 94; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                    1614 AAAAAAAA 1622
                                                                                                                                                                                                                                                                                                                                                                                    561 AAAAAAAA 569
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CITY: Ithaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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   , MULECCEL , US-08-554-659-11
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-103-429A-2
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                                                                     Query Match
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                                                                                              1521 CAACAAATGTTTTAGGAGATTACAAATCCATGGGAAGATGTATCAAACTCATCTCTCTAT 1580
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                                                                                                                                        2721 CAACAAATGGTTAAGAAAAAAAAGGATTTCTTAAAAATGTATTATTATAAAATGTGTAA 2780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MAKAR17
LOCATION: 945..968
OTHER INFORMATION: region corresponding to oligonucleotide MAKAR17
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                                                 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: KARMI, Mansour
APPLICANT: BARTHELS, Nathalie
APPLICANT: BARTHELS, Nathalie
APPLICANT: GAGGAIeve
TITLE OF INVENTION: PATHOGEN-INDUCED PLANT PROMOTERS
FILE REFERENCE: 6201-0014
CURRENT APPLICATION NUMBER: US/09/341,678
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: PCT/EP98/00388
EARLIER FILING DATE: 1998-01-19
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 5
LENGTH: 4160
                                                                                                                                                                                  46;
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2.2%; Score 36.4; DB 4;
Best Local Similarity 58.2%; Pred. No. 1.2;
Matches 64; Conservative 0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1418..1570
; OTHER INFORMATION: putative open reading frame
US-09-341-678-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: insertion point of T-DNA OTHER INFORMATION: insertion in the line ARMI
                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 90, Application US/08906769 Patent No. 6077687 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09341678 Patent No. 6252138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Arabidopsis thaliana
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NAME/KEY:
LOCATION: 1444..1445
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1439 TTCATCAATAGTCTCCATGTGAGGAGCCCTTTGTAAGAAAAAAGTGGTATCAATGTATAA 1498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    709 TTTACCAATGTTGCTCATTTRGTGGATTGGATTCAAGAACATACTGGATTGGAATTGTAA 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            769 AAATAAAACTCAAACTAAAAAAAAAATAATTTAATTGCACTGAAAAATTTTTCAAGAAAA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Sliver, Gary
APPLICANT: Sliver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 2.2%; Score 35.8; DB 3; Length 894; Best Local Similarity 49.7%; Pred. No. 0.81; Matches 91; Conservative 0; Mismatches 92; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "At pos. bp 560, change G to
N. At pos. aa 187, substitute Xaa.
                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 25.020
REGISTRATION NUMBER: 2618-25-C2-3
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
                                                                                                                                                                                                                    1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                     2: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-08-817-795-90
Sequence 90, Application US/03817795
Patent No. 6139840
GENERAL INFORMATION:
                                                                                                                                                                                                        Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Grieve, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: ; ; OTHER INFORMATION: ; ; US-08-906-616-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                       Colorado
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     709 TTTACCAATGTTGCTCATTTTGTGGATTGGATTCAAGAACATACTGGATTGGAATTGTAA 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.2%; Score 35.8; DB 3; Length 894; Best Local Similarity 49.7%; Pred. No. 0.81; Matches 91; Conservative 0; Mismatches 92; Indels
                                           FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "At pos. bp 560, change G to N. At pos. aa 187, substitute Xaa."
                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
                                                                                     NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILLING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-906-616-90
; Sequence 90, Application US/08906616
; Patent No. 6121035
; GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
    Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 90.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 894 base pairs
TYPE: nucleic acid
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                       APPLICANT: Silver,
TITLE OF INVENTION:
TITLE OF INVENTION:
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STATE:
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ò g Search completed: November 5, 2001, 18:04:15 Job time: 15055 sec

889 AAA 891

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APPLICANT: Arfsten, Ann
APPLICANT: Dale, Beverly
APPLICANT: Dale, Beverly
APPLICANT: Stiegler, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
CORRESPONDENCES: 119
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                            CITY: Deriver
STATE: Colorado
COMPRY: USA
ZIP: BO203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
RILING DATE:
RECEIVED TOWN NUMBER: PCT/US95/14442
                                                                                                                                                                                                                                                                                          E: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
                                                          Heath, Andrew W.
Yamaka, Miles Yamanaka
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187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303 863-923
INFORMATION FOR ESC ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                     Hunter, Shirley Wu
Frank, Glenn R.
Rushlow, Keith E.
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Best Local Similarity 49.7;
Matches 91; Conservative
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STREET: 17
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LOCATION:
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; LOCATION:
US-08-817-795-90
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Human lung tumour

Malaria-specific g SERP gene. Plasmo

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Searched:

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Minimum DB seq Maximum DB seq

Database

Human cancer assoc Nucleotide sequenc Nucleotide sequenc Human TGF-beta rec Nucleotide sequenc Nucleotide sequenc

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Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; gentiana triflora; Petunia hybrida; Perilla ocimoides; scenecio cruentus; Lavandula angustifolia; ds.
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//product= Aromatic acyl transferase.
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/transl_except= ATC encodes
1322..1324
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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Result No.

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transforming
ering colour
                                         Mizutani
                                                                            coding for aromatic acyl transferase - for transf
h produce anthocyanin pigments and thus altering
of flowers
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                                         Kusumi
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                                         Fukui
ıra K;
                                             Tanaka Y, Yonekura
96JP-0046534.
95JP-0067159.
95JP-0196915.
                                         'n
                                         Fujiwara
                          (SUNR ) SUNTORY LID
                                                            1996-393401/39
                                                                  AAW04723
30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
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                                               Nakao M,
                                        Ashikar1
                                                                   P-PSDB;
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plants tone,

Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.

T; 0 other; 477 C; 313 G; Sequence 1622 BP; 478 A; 354

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   1622;
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  Length
                 Indels
  17;
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Score 1607.6;
Pred. No. 0;
0; Mismatches
99.1%;
illarity 99.4%;
Conservative 0
Query Match
Best Local Similarity
Matches 1613; Conserv
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840 840 GCAACTIGTAGGAAATGAAGGGTTGTCGGTAGCTGCAACCGCCATCGGAGATGCTATCCA TAAGAGGTTACATGACTACGAAGGAATTCTGAGAGGAGATTGGATATCGCCGCCCCGATC GCATGATTTGATGCAGATTTGGTTGGGGAAAGCTTGAAAAGCATGAATCTGTTCAAC gcatgattttgatgcagattttggttggggaaagcttgaaaagcatgaatctgtttcaac GCTCAAATCTCAGGGCACACCTACTGTTCTAAATCCAGCAATTTCTAAAGATGAAGTTCG AGCCACCTTCATCCTACACCCTATTGATATCATGAAGCTCAAGAAATTCATTTCGTCAAA GGATAAACATGCAGCAAACTTATGTTCTTCATCAACTGCCGACAACGTTTTGCTCCGCC ggataaacatgcagcaaacttatgtgctttcatcaactgccgacaacgttttgctccgcc GATACCTCAAAATTACTTTGGAAATTGCATAGTGCCTTGTATGGTGGGATCGACTCATGA AACATCTGCGGCACCAAGGTCGACGCTCATTTATGTCGTTGGATCCGCACAACGCAATGT TAATCCTTCGGCAACACTAATTTTGATCTCTCGGTCCAGAAGATTTAAAAGGAGCACTTGA GCTTGGCATTTCTTTGCCTAAGAATAGGATGGACGCATTTGCCACCATTTTACGAATTT gcttggcatttctttgcctaagaataggatggacgcatttgccaccatttttacgaattt CATCAATAGTCTCCATGTGAGGAGCCCTTTGTAAGAAAAAGTGGTATCAATGTATAAAA AAGACAGACAAGTTATGATGCAACAAATGTTTTAGGAGATTACAAATCCATGGGAAGATG ΑA 1021 1021 1081 1141 1141 1201 1321 1381 1441 601 721 781 901 961 1081 1201 1261 1261 1321 1381 1441 1501 1561 1561 661 199 721 781 841 901 961 1501 1621 601 g 8 g QQ ò g ò ò 8 οy ò g δ g δ δý g δ qq οy g δ 임 δ g ò g ò g à g ŏ qq ò

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1079 GAGCAACTTGTAGGAAATGAAGGGTTGTCGGTAGCTGCAACCGCCATCGGAGATGCTATC 1138
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   CTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTAGAT
                                     183 ctctctaaaactctcatacacttcttccctctctcatgcaatttaatctacccttca---
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                                                                          299 TCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATT
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                                                                                                                                                                                  Aromatic acyl transferase; transformation; anthocyanin pigment; plante; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.4%; Score 218; DB 17; Length 1479; 50.8%; Pred. No. 3.1e-46; .ive 1; Mismatches 661; Indels 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
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/*tag= a
/product= Aromatic acyl transferase.
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                                     standard; cDNA to mRNA; 1479
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                                                                                                                                                                                                                                                                           Perilla ocimoides (Clone pSAT208)
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Nakao M, Tanaka Y, Yonekura K;
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95JP-0067159.
95JP-0196915.
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P-PSDB; AAW04725.
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1439 TTCATCAATAGTCTCCATGTGAGGAGCCCTTTGTAAGAAAAAGTGGTATCAATGTATAA 1498
                                                                                                             Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
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                                   GAGCTTGGCATTTCTTTGCCTAAGAATAGGATGGACGCATTTTGCCACCATTTTACGAAT
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ura K;
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6..1415
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Nakao M, Tanaka Y, Yonekura
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P-PSDB; AAW04722.
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Sequence 1703 BP; 512 A; 353 C; 356 G; 482 T; 0 other;

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                                                      TCAAAGTTCTTGAGAAATGCCGTGTTGCGCCACCACCGGAC---GCCGTCGCCGAGTTTA 113
                                                                                                          CAGTCCCACTGTCGTTTTTCGACATGCGTTGATCTCTGATGCAGAACACCATCTGC 173
                                                                                                                         AATCGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGC 290
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                              Gaps
                                                                    ATTICTACAGATICCGCCAICCTIGICCCAA---CICTAAAITITAICAITCAICCAITA
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                           Indels
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 Score 190.8; DE
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"" Lanaka Y, Yonekura K;
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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAM37308-T37313. NOTE: This sequence is supposed to cross reference with the protein described in AAM04727. however there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide given in the specification and described in AAW04727 that the indexer decided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AATGCCGTGTTGCGCCACCACCGGACGCCGTCGCCGAGTTTACAGTCCCACTGTCGTTTT 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                        plants
tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 tgaacattctcgaacatgcccgaatatcggccccctcgggcaccatcggccatcgctcgt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.6%; Score 139.8; DB 17; Length 1508; Best Local Similarity 48.7%; Pred. No. 3.2e-26; Matches 677; Conservative 0; Mismatches 642; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                 DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
                                                                                                                                                                           Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 tgaaagggtggacttcgattattcaatctggtgtagat-------
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                                                                                                                                                                               Kusumi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 69-72; 94pp; Japanese
                                                                                                                                                                               Fukui Y,
                                                                                                                                                                                                               Tanaka Y, Yonekura K;
95JP-0067159.
95JP-0196915.
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                                                                                                           (SUNR ) SUNTORY LTD
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   17-FEB-1995;
29-JUN-1995;
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                                                                                                                                                       TAAGAGAAGATGGAAGAGGATAAACATGCAGCAAACTTATGTGCTTTCATCAACTGCC 1001
                                                                       762
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                                                                      gtoccactgataaagttcggtcaacgtttgtgttgacccgaactaatatcaatctactaa
                                                                                        AGAAATTCATTTCGTCAAAAATCGCAACTTAACCGGTAGTAGTAATTATAATCTGTCAA
                                                                                                TGGTGGGATCGACTCATGAGCAACTTGTAGGAAATGAAGGGTTGTCGGTAGCTGCAACCG
                                                                                                                                                                                                                                                                                                                                                                          agtatgagactgtttcaataga---ctataatacgtcgatttctataaatgcaagcaaaa
       TCTACAATGAAAGAAAACTGCTCAAATCTCAGGGCACACCTACTGTTCTAAATCCAGCAA
                                      643 atgaaaataagttgagacatacaaggctcgaaagtttttataaaccttcgagccttgttg
                                                                                                                       CTTTCACGGTGACATCTGCACTGGACATGCTTGTCGAAATCATTAGACACGGTCG
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                                                       TTTCTAAAGATGAAGTTCGAGCCACCTTCATCCTACACCCTATTGATATCATGAAGCTCA
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
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6.0%; Score 96.8; DB 2
Best Local Similarity 1.0%; Pred. No. 2.8e-15;
Matches 8; Conservative 453; Mismatches 3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 127; 159pp; English
                                                                                                                                                                                             (CLIN-) CLINICAL MICRO SENSORS
                                                                                                         26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                    26-JUL-2000; 2000WO-US20476
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01-FEB-2001
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24-APR-2001 (first entry)
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1517 GATGCAACAATGTTTTAGGAGATTACAAATCCATGGGAAGATGTATCAAACTCATCTCT 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     977 AACTTATGTGCTTTCATCAACTGCCGACAACGTTTTGCTCCGCCGATACCTCAAAATTAC 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          857 GGTAGTAGTAATTATAATCTGTCAACTTTCACGGTGACATCTGCACTGGATCTGGACATGC 916
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                                                                          Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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2000US-0190259.
                                                                                                                                            DNA; 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monitoring gene expression
                                                                                                                                                                                  (first entry)
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                                                                                                                                            AAF58254 standard;
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1217 AGGTCGACGCTCATTTATGTCGTTGGATCCGCACAACGCAATGTGCATGATTTGATGCA 1276
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                                                                                                                           TTTGGAAATTGCATAGTGCCTTGTATGGTGGGATCGACTCATGAGCAACTTGTAGGAAAT
                                               1097 GAAGGGTTGTCGGTAGCTGCAACCGCCATCGGAGATGCTATCCATAAGAGGTTACATGAC
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17-MAR-2000; 2000US-0190259
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                        The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                    GGTAGTAGTAATTATAATCTGTCAACTTTCACGGTGACATCTGCACTGATCTGGACATGC 916
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                                                                                                                                                          6.0%; Score 96.8; DB 22;
.0%; Pred. No. 2.8e-15;
.ve 453; Mismatches 305;
                                                                                                                             Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                       Example 6; Page 127; 159pp; English.
                                                                                                                                                                               Conservative 453;
                                                                                                           monitoring gene expression.
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Best Local Similarity 1.0%;
Matches 8; Conservative 4
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AACTTATGTGCTTTCATCAACTGCCGACAACGTTTTGCTCCGCCGATACCTCAAAATTAC 1036
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L.0%; Pred. No. 2.8e-15;
Lve 453; Mismatches 305;
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17-MAR-2000; 2000US-0190259.
DNA; 936
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Best Local Similarity 1.0%;
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                                                                                                                                                                                                                  gene expression; ss
  standard;
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AAF58259
                                               AAF58259;
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Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

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1217 AGGTCGACGCTCATTTATGTCGTTGGATCCGCACAACGCAATGTGCATGTTTGATGCA 1276
                                               1277 GATTTTGGTTGGGGAAAGCTTGAAAAGCATGAATCTGTTTCAACTAATCCTTCGGCAACA 1336
                                                                                            1337 CTAATTTTGATCTCTCGGTCCAGAAGATTTAAAGGAGCACTTGAGCTTGGCATTTCTTTG 1396
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                                                                                                                                                                 1397 CCTAAGAATAGGATGGACGCATTTGCCACCATTTTTACGAATTTCATCAATAGTCTCCAT
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression; ss
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                                                                                                                                                                                                                                                                                                                                                                                  AGGTCGACGCTCATTTATGTCGTTGGATCCGCACAACGCAATGTGCATGATTTTGATGCA 1276
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                                                               857 GGTAGTAGTAATTATAATCTGTCAACTTTCACGGTGACATCTGCACTGATCTGGACATGC
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            22;
         6.0%; Score 96.8; DB;
llarity 1.0%; Pred. No. 2.8e-15;
Conservative 453; Mismatches 30
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Query Match
Best Local Similarity
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1397 CCTAAGAATAGGATGGACGCATTTGCCACCATTTTTACGAATTTCATCAATAGTCTCCAT 1456
                                                                                                                               1517 GATGCAACAAATGTTTIAGGAGATTACAAATCCATGGGAAGATGTATCAAACTCATCTT 1576
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                                128 TTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTTCTACAGATTC 187
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gene expression; ss.
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Matches 12; Conservative 451;
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2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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ilarity 1.0%; Pred. No. 2.8e-15;
Conservative 453; Mismatches 305;
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gene expression; ss.
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1ve 451; Mismatches 312;
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WPI; 2001-159728/16.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
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17-MAR-2000; 2000US-0190259.
                                                                                                AAF58257 standard; DNA; 936
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	E12754 1622 bp DNA
	Gentianatriflora mRNA for acy
ACCESSION	E12754
	E12754.1 GI:3251586
KEYWORDS	JP 1997070290-A/2.
	unidentified.
ORGANISM	unidentified
REFERENCE	1 (bases 1 to 1622)
AUTHORS	Ashikari, T., Tanaka, Y., Fujiwa
	Mizutani, M.
TITLE	GENE CODING PROTEIN HAVING ACT
JOURNAL	Patent: JP 1997070290-A 2 18-1
	SUNTORY LTD
COMMENT	OS Gentianatriflora
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	TOSHIHIKO, TANA
	ASAHIRO,
	PI FUKUI YUKO, YONEKURA KEII
	C12N15/09, A01H1/00, C07H21/0
	C12R1:865),
	PC (C12N9/10,C12R1:19);
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           24-JUN-1998
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SHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                              rara,H., Nakao,M., Fukui,Y.,
Kusumi,T.
YL GROUP TRANSFER ACTIVITY
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Gentlanatriflora mRNA for acyltransferase, complete cds.
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/clone='pGAT106'
35. 1474
/product='acyltransferase'
Location/Qualifiers ; u 100.0%; Score 1622; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 7.1622 /organism="unidentified" /db_xref="taxon:32644" a 345 c 322 g 477 477 Best Local Similarity Matches 1622; Conserv ø CDS FT FT Query Match source BASE COUNT ORIGIN 181 (241 121 181 301 301 FEATURES ò ò d g à g δ Db ŏ q ò

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Yoshikazu Tanaka, Suntory Ltd., Institute for Fundamental Research, Wakayama-dai 1-1. Shimamoto, Osaka 618-8503, Japan (E-mail:Yoshikazu_Tanaka@suntory.co.jp, Tel:81-75-962-8807, Fax:81-75-962-8262)
Yonekura-Sakakibara,K., Tanaka,Y., Fukuchi-Mizutani,M.,
Fujiwara,H., Fukui,Y., Toshihiko,A., Yamaguchi,M. and Kusumi,T.
Molecular cloning and biochemical characteization of
hydroxycinnmamoyl-CoA:anthocyanin
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2 (bases 1 to 1622).
2 (hases 1 to 1622).
Direct Submission Yonekura-Sakakibara, K.
Direct Submission (21-APR-1999) to the DDBJ/EMBL/GenBank databases.
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/db_xref≔"taxon:55190"
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100.0%; Pred. No. 0;
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Gentiana triflora GAT106 mRNA for acyltransferase homolog, complete
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Gentiana triflora cDNA to mRNA.

Gentiana triflora cDNA to mRNA.

Gentiana triflora

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Gentianales; Gentianaceae; Gentiana.
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
C12R1:865),
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                                 1501 AAGACAGACAAGTTATGATGCAACAAATGTTTTAGGAGATTACAAATCCATGGGAAGATG 1560
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ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI,
                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 1479)
Ashikari, T., Tanaka, Y., Fujiwara, H., Nakao, M., Fukui, Y.,
Yonekura, K., Mizutani, M. and Kusumi, T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070290-A 4 18-MAR-1997;
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Best Local Similarity 50.8%; Pred. No. 4.6e-44;
Matches 741; Conservative 1; Mismatches 661;
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/organism="unidentified"
/db_xref="taxon:32644"
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18-MAR-1997
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JP 1997070290-A/4.
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/product.anthocyanin acyltransferase*
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315 c 331 g 411 t
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Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Keiko Y
Sakakibara. Suntory Research Center. Fundamental Research, Plant
Biotech; Shinamotory Research Wakayamadal, 1-1-1, Mishina-gun, Osaka
618-8503, Japan (F-mail:Keiko_Sakakibara@suntory.co.jp,
Tel:+81-75-962-8807, Fax:+81-75-962-8262)
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Perilla frutescens leaf CDNA to mRNA.
Perilla frutescens
Bernaryota viridiplantaes Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
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                                                                                                                                                                                      ATTGATGGGGAGAAATATGCAATGACRCTTTGTAAAGCCAGGGATTTCGAAGGAGGATTG 1268
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                                                                                         GAGGTTTGCTTTGCCTAAGGACAAATGGATGCTTTTTGCTTGTTTTTCACTG
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Sakakibara,K.Y., "anaka,Y., Mizutani,M.F., Fujiwara,H., I
Ashikari,T., Yamaquchi,M. and Kusumi,T.
Molecular and biochemical characterization of a novel
hydroxycinnamoyl_coA: anthocyanin 3-0-glucoside-6
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/tissue_type="leaf"
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Sakakibara, K.Y. and Tanaka, Y.
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                                                                                                CTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTAGAT
                                                                                                               GCAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCCGTTAGG
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                                         AGATTCCGCCATCCTTGTCCCAAC - - - TCTAAATTTATCATTCATCCATTAAATCGTCC
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PPNRGIAVALTAHHSIADAKSFVMFINAMAYINKFGKDADLLSANLLPSFDRSIIKDL
YGLEETFWNEMODVLENFSRFGSKPPRFNKVRATYVLSLAETOCKLKNVTNLKGSEPT
YRTTFFTHACYVWTCWYKSKDDVVSESSNDENELEYFSFTADCRGLLTPPCPPNYF
GNCLASCYAKTHRELYGDKGLLLYANAAIGEAIEKRHHNEKGYLADAKTWLSSENGIP
SKRFLGITGSPKFDSYGVDFGWGKPAKFDITSVDYAELIYVIQSRDFEKGVEIGVSL
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SLLFYDFPYPRTHFLDTVIPNLKASLSLTLKHYVPLSGNLLMPIKSGEMPKFQYSRDE
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Fujiwara,H., Tanaka,Y. and Kusumi,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (sites)
Fujiwara,H., Tanaka,Y., Yonekura-Sakakibara,K.,
Fujiwara,H., Tanaka,Y., Yonekura-Sakakibara,K.,
Fukuchi-Mizutani,M., Nakao,M., Fukui,Y., Yamaguchi,M., Ashikari,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB010708 1679 bp mRNA PLN 20-FEB-1999
Gentiana triflora mRNA for Anthocyanin 5-aromatic acyltransferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (22-JAN-1998) to the DDBJ/EMBL/GenBank databases.
Hiroyuki Fujiwara, Suntory LTD., Inst. of Fundamental Research;
1-1-1, Wakayamadai, Shamamoto-cho, Osaka 618-0024, Japan
(E-mall:Hiroyuki_Fujiwara@suntory.co.jp, Tel:+81-75-962-8807,
1101 CGTAAAGC-----GTTGCAGAAATCATATTTTCGGTGGCAGGATCGAGCAAG 1148
                                                                                                   1149 CTAGATCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAGCAAGAATATTGTCG 1208
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                                               GTGCATGATTTTGATGCAGATTTTGGTTGGGGAAAGCTTGAAAAGCATGAATCTGTTTCA
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/product="Anthocyanin 5-aromatic acyltransferase"
/protein_id="BAAA74428.1"
/db_xref="GI:4185599"
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Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
Gentiana triflora
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/db_xref="taxon:55190"
/clone="pGAT4"
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/db_xref='taxon:32644"
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strandedness: Double;
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                               48;
        Length 1679
                               Indels
         DB 12;
        Score 189.2; DB 12;
Pred. No. 7.8e-37;
0; Mismatches 618;
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Best Local Similarity 52.2%;
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                              GCGTTGCAAAAGCAACACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTG 1086
                                                                     CAAAAACTIGGITAICGGAATCTAAI....-.GGAATCCCTICAAAAAGAITTCTCG 1197
                                                                                                                                                                                                                                        TIGGAICCGCACAACGCAA'TGTGCAIGAITITGAIGCAGAITITIGGTTGGGGAAAGCTTG 1298
                                                                                                                                                                                                                                                                                                                                  1299 AAAAGCATGAATCTGTTTCAACTAATCCTTCGGCAACACTAATTTTGATCTCTCGGTCCA 1358
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PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691:
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
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                                               CCGCCATCGGAGATGCTATCCATAAGAGGTTACATGACTACGAAGGAATTCTGAGAGGAG
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/product='acyltransferase precursor'
9. 1412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E12753 1703 bp DNA Gentianatriflora mRNA acyltransferase,complete cds. E12753.1 G1:3251585
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/organism='Gentianatriflora'
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/tissue_type='petal'
/clone='pGAT4'
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                                                                                57 TCAAAGTICITGAGAAATGCCGTGTTGCGCCACCACCGGAC---GCCGTCGCCGAGTTTA 113
                                                                                                                                                                                                                                                                                            345 TTTCTTTAACAATTGCAGAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGA 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                         502 TAGCCGTGGCTCTGACGGCACATCATTGCAGATGCTAAAAGTTTTGTAATGTTCA 561
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                                                              Gaps
                                                                                            85 CGCTACCGGTAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTC
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                                        Length 1703;
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                                         DB 10;
                                       Score 189.2; DB 10;
Pred. No. 7.9e-37;
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ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
MASAHIRO,
                                                                  GTATGGTGGGATCGACTCATGAGCAACTTGTAGGAAATGAAGGGTTGTCGGTAGCTGCAA
                                                                                                                                                     1119 CCGCCATCGGAGATGCTATCCATAAGAGGTTACATGACTACGAAGGAATTCTGAGAGGAG
                                                                                                                                                                              1087 CAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATG
                                                                                                                                                                                                                                              1179 ATTGGATATCGCCGCCCCGATCAACATCTGCGGCACCAAGGTCGACGCTCATTTATGTCG
                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1508)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 5 18-MAR-1997;
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Location/Qualifiers
1. 1508
/organism-"unidentified"
/db_xref-"taxon:32644"
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/clone='pCAT48'
1.1367
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JP 1997070290-A/5
18-MAR-1997
30-JAN-1996 JP 1996046534
17-FEB-1995 JP 95P 67159
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PC (C12N9/10,C12R1:19);
CC strandedness: Double;
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Senecio cruentus mRNA
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JP 1997070290-A/5.
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Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.
                                                                                                                                  CCATCGGAGATGCTATCCNTAAGAGGTTACATGACTACGAAGGAATTCTGAGAGAGTT 1181
                                                                                                                                                      1102 CGAGATGGCATGAACCTTT?CATGATCCCGG------CTAGGAAGATTGGTGTTGCTG 1152
                                                                                                                                                                                                                                                                                    GATCCGCACAACGCAATG9GCATGATTTTGATGCAGATTTTTGGTTGGGGAAAGCTTGAAA 1301
                                                                                                                                                                                                                                                                                                        AGCATGAATCTGTTTCAACTAATCCTTCGGCAACACTAATTTTGATCTCTCGGTCCAGAA 1361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hyman R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W. Direct Submission Submitted (21-JUL-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 178273)
Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T., Rurdi, O.B., Conway, A. B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 1782/3: contig of 178273 bp in length.
 982 TCCCGACCTTAAAAAATGTCGTTTTGACTAGCGAAAATGGGTATGCACTTGGTGCTAAAG
                                                                                                                                                                                                            1182 GGATATCGCCGCCCCGATCAACATCTGCGGCACCAAGGTCGACGCTCATTTATGTCGTTG
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On Aug 12, 2000 this sequence version replaced 91:8810450.
* NOTE: This is a "working draft" sequence. It currently
consists of I contigs. Gaps between the contigs.
* are represented as runs of N. The order of the pieces
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/organism="Plasmodium fa
/db_xref="taxon:5833"
/chromoscome="12"
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Plasmodium falciparum
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/clone="3D7"
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HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                              TCCCACTGTCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATT 176
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                                                                                                                  Gaps
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                                                                                                                 72;
                                                                          Length 1508,
                                                                                                                 Indels
                                                                        Score 139.8; DB 10;
Pred. No. 1.9e-24;
0; Mismatches 642;
 477
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 296
                                                                          8.6%;
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                                                                                                               677; Conservative
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                                                                                           Similarity
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 442
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BASE COUNT
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Best Local Similarity
Matches 86; Conserv
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AC004688/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 4 unordered places.
                                                                                                                                                                               76638 AATAAATAAAATAAAAATAAAAATATGTTAAAAAAAAAGAATTCCGAATTTTAAATGC 76579
                                                                                                                                                                                                                                            76578 ITTAAAAAATGGTCAAAAATTTATATTTATGAATATTTTACAAAATTGGGAAAAAAT 76519
                                                                                                                                         1490 AATGTATAAAAAAGACAGACAAGTTATGATGCAACAAATGTTTTAGGAGATTACAAATCC 1549
                                                                                                                                                                                                                         Gaps
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HTG; HTGS_PHASE1.
malaria parasite P. falciparum.
Plasmodium falciparum falciparum falciparum a falciparum Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases I to 205429)
Hyman, R.W., Fung, E.L., Oliv, F., Rowley, D., Mao, J., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently ronsists of 4 contigs. The true order of the pieces to not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T (bases 1 to 205429)
Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
                                                        Length 178273;
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132469: gap of unknown length
19227: contig of 59758 bp in length
192427: gap of unknown length
203864: contig of 11437 bp in length
204064: gap of unknown length
205429: contig of 1365 bp in length.
                                          Score 50.4; DB 6u; ____
Pred. No. 0.095; ____trhes 51; Indels
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                                                        Query Match 3.1%;
Best Local Similarity 61.4%;
Matches 81; Conservative
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Best Local Similarity 58.3
Matches 88; Conservative
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On Aug 12, 2000 this sequence version replaced gi:8810452.

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                          AC004688 169794 bp DNA HTG 12-AUG-2000
Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
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                                                                              1476 AAAAAAGTGGTATCAATGTATAAAAAAGACAGACAAGTTATGATGCAACAAATGTTTTAG 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG: HTGS_PHASE1.

malaria parasite P. falciparum.
Plasmodium falciparum.
Bukaryota: Alvediata: Apicomplexa: Haemosporida; Plasmodium.

(bases 1 to 169794)
Hyman, R.W., Fung, P.L., Qin, F., Rowley, D., Mao, J., Tamaki, T., Rurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 169794)
Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
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830 44029: gap of unknown length
030 87202: contig of 43173 bp in length
403 87402: gap of unknown length
825 95024: contig of 7422 bp in length
025 169794: contig of 74770 bp in length
1.169794
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/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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Pred. No. 0.12;
0; Mismatches
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                                                                                                                                                          1592 CAATTGTTTAAAAAAAAAAAAAAAAAAAAA 1622
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atb6 gene; atb9 gene; Arpase Subunit 6; Arpase subunit 9; cob gene; cox1 gene; cox2 gene; cox3 gene; cytochrome b; cytochrome oxidase subunit 1; cytochrome oxidase subunit 1; cytochrome oxidase subunit 2; cytochrome oxidase subunit 3; nad1 gene; nad3 gene; nad3 gene; nad4 gene; nad5 gene; nad5 gene; nad6 gene; nad8 gene; nad8 gene; nad8 gene; nad8 gene; nad8 gene; nad9 gene; nas9 gene; ris2 gene; ris2 gene; ris2 gene; ris4 gene; ris5 gene; ris5 gene; ris6 ge
                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion Scenedesmus obliquus
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlorococales; Scenedesmaceae; Scenedesmus.

I (bases 1 to 42781)
Kuck, U., Godehardt, I. and Schmidt, U.
A self-splictny group II introm in the mitochondrial large subunit
FRNA (LSURRNA) gene of the eukaryotic alga Scenedesmus obliquus
Nucleic Acids Res. 18 (9), 2691-2697 (1990)
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KNLYYNLLFKKCKDYSKDSFFCIFYNIKKSLL"
                              16S ribosomal RNA; 16S rRNA gene; 23S ribosomal RNA; 23S rRNA gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 42781)
Winkler,W. and Kuck,U.
The green alga Scenedesmus obliquus
mitochondrion: molecular characterization of the in vitro splicing
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Kuck, U., Jekosch, K. and Holzamer, P.
Na sequence analysis of the complete mitochondrial genome of the green alga scenadesmus obliquus: evidence for UAG being a leucine and UCA being a non-sense codon
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Submitted (05-MAY-2000) Jekosch K., Ruhr-Universitaet Bochum, I fuer Allgemeine und Molekulare Botanik, Universitaetsstr. 150, D-44780 Bochum, GERMANY
On MAY 23, 2000 this sequence version replaced gi:7573226 gi:7160201 gi:71619793 gi:7573572 gi:13633.

Location/Qualifiers
1. 42781
/organism="Scenedesmus obliquus"
/crganeil="mitochondrion"
/strain_"KS3-2"
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Botanik, Ruhr-Universitaet Bochum, Postfach 10 21 48,
Universitaetsstr:150, D-44780 Bochum
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/gene="tENA-Ile"
/product="transfer RNA Ile"
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/db_xref*"GI:7711034"
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/gene="crf76"
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/country="Germany"
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/transl_table=22
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5 (bases 1 to 42781)
Jekosch, K.
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Submitted (21-MAY-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

On Apr 2, 1999 this sequence version replaced gi:4337173.

* NOTE: This is a "working draft" sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
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HTG; HTGS_PHASE1.
Palandium falciparum.
Plasmodium falciparum falciparum falciparum falciparum
Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 196149)
Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B., Conway, A.B.
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                                                                                                                                                                                                                                                            :004709 196149 bp DNA HTG 01-APR-1999 asmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS
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Scenedesmus obliquus complete mitochondrial genome.
X17375 AJ271733 AJ272528 AJ277429 AJ400708
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47632 47831: gap of unknown length
47832 179129: contig of 131298 bp in length
179130 179329: gap of unknown length
179330 196149: contig of 16820 bp in length.
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/db_xref="taxon:5833"
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Unpublished
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CDS

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/product="NADH dehydrogenase subunit 4L"
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/gene="trna-tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTEYVGVLLYIAIAVGLGIVILFRSYKVRPRRLDLEKATAYECG
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Scenedesmus obliquus strain UTEX 78 mitochondrion, complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /anticodon-(pos:10079. .10081, aa:Leu)
10046. .10127
/gene-"tRNA-Leu"
10133. .10203
/gene-"tRNA-Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /anticodon=(pos:10165. .10167,aa:Arg)
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/gene="tRNA-Tyr"
10046. .10127
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/note="codon recognized: CUU"
/product="tRNA-Leu"
                                                                                                                                                                                                                                                                           /note="codon recognized: UAC" /product="tRNA-Tyr"
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10213. 10284
/gene="tRNA-11e"
/note="codon recognized: AUC"
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10486. .10839
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10486. .10839
/gene="nad3"
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/gene="nad4L"
                 /gene="nad4L"
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                                                                                                                                                                                               /protein_1d="CAB90359_1"
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VYTYDDLVSKPALTVKVTGRQWYWSYAMNEHVQMNLSQQAKDLLLQS"
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/db_xref="61:711053"
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/Itranslation="1711NA9"
/ITRANSAGSACVTILGMGTSTLLSY
/ITRANSAGSAVULSLGSWFCAHTVTVEWILCFDPLSAAMMVTVCTVSFCVHIYSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLEFLGAGYVIHACADVQDMRRSGGAHASLPLAWTCLLXGSLSLLGWPFLAGYYSKDA
HIABLSWATPGSAAALGHLILMYVACLTSAYSRYBLIAVFYAPNNARKSENTPGYPLT
MAVPLCILALGSIFRGYLLSDALIGWGTDFFANSITRSPATTQAVRSHMIPVMISALP
LATVGAGLLLAYVEVWPLPYCAESYWKRPYLPLQARWGFDLWNNQQISWKVLGAGGSAS
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WVGAVTSLMRRTMGLVQNDVKRVIAYSTCSQLGYMVVALSLSHYGLAMYHLMTHACFK
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VAGLTENLLVDYKTLTLRVLLISICL"
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/gene="nad5"
join/con
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                                                                                                                                                                                                                                                                                    VFGLKIPGKAILLSVRQQDQELGQVKSL"
                                                                                                                                                                                                                                                                                                                                                                                          /function="respiratory chain"
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complement(3340. .3732)
/gene="orf130"
                                                                          complement(3340. .3732)
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/note="group I intron"
                                                                                                                /function="unknown"
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                                                                                                                                          /codon_start=1
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/gene="orf90"
6853. .7125
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/gene="cox2"
4893. .5342
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SGDINICLGNNVKGEDHTFVNMPYDKKKWNEIRKSTNNNYNNINRDKRNTHRSLKNVR
IINIKHKNISYVICKNYLKKGKNYYERRMLKNMNLKYNILKINKYILSCNNIYKYAKM
                                       AL035475. 6 GI:6562702
Albosomal protein; replication A protein; ribosomal processing protein; ribosomal protein; rifin; transcription factor; var.
malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases I to 234112)
Devlin,K., Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M. and Barrell,B.
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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NKEKPNDDINIVKMKKRRTYIFINKTYKLFIHNYKNISFKFENLMRKHFVAKYDYIF
KKLSYYITLKKEIDLCKLYMYDMNALEILDKNLDIHIKENKLIQNLHCTINLREIENI
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KIYNEKSNLINIINNKNDIMKTTDVKNDKTLKDDTIERINOKVVKTKKNHLINEEEKN
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KKNITNEKMELEKEIKNFSNEKITIEKEKONISNDKITLEKEIONIRNEKMTLEKEIO
NISNDKITIEKEIKNFRNDKITLEKEIKNFRNDKMTLEKEIKNFSNDKITLEKEIONI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB10 1sA, UK
On Dec 12, 1999 this sequence version replaced gi:5731898.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is not the entire insert of clone MAL4P2: It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring
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> 1130 aa, contains NKSKPDD repeat sequence"
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/db_xref="GI:6562704"
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/db_xref="SPTREMBL:09U0M1"
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/note="G(7)-tract upstream of MAL4P2.01"
Plasmodium falciparum MAL4P2, complete sequence
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5644. .6063
/gene="MAL4P2.02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'translation="MVQARKLIGAGSALIALAGVGAGIGIVFGALIQRARRNPQMAKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=22
/product="ATP synthase F0 subunit 9"
                                                                              (anticodon=(pos:8676. .8678,aa:Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .9353, aa:Ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /anticodon=(pos:9594, .9596,aa:Phe)
9562, .9633
gene="trnF(gaa)"
                                                                                                                                                                                                                                                                                 .8784, aa:Pro)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anticodon=(pos:9676. .9678, aa:Glu)
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/db_xref="GI:8099195"
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/gene="trnS(gcu)"
/product="tRNA-Ser"
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/product="tRNA-Phe"
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                                'gene≖"trnL(cag)"
'product="tRNA-Leu"
                                                                                                                                                                                                                                                       product-"tRNA-Pro"
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/gene="trnE(uuc)"
9767. | 1004
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                                                                                                                                            /gene="trnL(cag)"
8749. .8821
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/gene="trnP(ugg)"
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/gene="trnP(ugg)"
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/gene="orf345"
9767.
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/gene="orf345"
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                                                                                                                                                                                                                                                                                                                                                                            3867. .9088
/gene="atp9"
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/gene="atp9"
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85; Conserv
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Best Local 9
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PFMAL4P2/c
LOCUS
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10379. 10384
/note="predicted donor sequence, cag/gtaaaa, for exon 11 of MALAP2.03"
10541. 10550
/note="predicted splice acceptor sequence for exon 12 of MALAP2.03"
10707. 10712
/note="predicted splice donor sequence, tat/gtatgt, for exon 12 of MALAP2.03"
10766. 10775
/note="predicted splice acceptor sequence for exon 13 of MALAP2.03"
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4040ne="MALALP2.04"
//note="MALAP2.04"
revised: added two 3' exons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(10868, .10972,11088, .11177,11367, .11617, 11727, .11794,11978, .12324))
/gene="MALAP2.04"
                                                                                                                                                                                                                             'note-"alternative splice acceptor sequence for exon 9 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAL4P2.03"
10019. .10024
foote="predicted splice donor sequence, cac/gtaaga, for exon 9.5 MAL4P2.03"
10160. .10169
foote="gredicted splice acceptor sequence for exon 10 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALAP2.33"
10251. .10256
/note="predicted splice donor sequence, aag/gtaata, for exon 10 of MALAP2.03"
10330. .10339
/note="predicted splice acceptor sequence for exon 11 of MALAP2.03"
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//note="predicted splice donor sequence, tat/gtatat, for exon 7 of MAL4P2.03"
8628. 8637
//note="predicted splice acceptor sequence for exon 8 of MAL4P2.03"
9610. 9615
                                                                                                                                  9610. 9615
/note='predicted splice donor sequence, acc/gtaaat, for exon 8 of MAL4P2.03"
9645. 9650
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/note="predicted splice acceptor sequence for exon 9 f
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Pred. No. 0.22;
0; Mismatches 50; Indels 0;
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/gene="MAL4P2.03"
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Best Local Similarity 61.2%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAL4P2.03"
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| Db 222675 AGCAAAAA 222667
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AC023268/c
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                                                                                           6787. :6792

/note-alternative donor sequence (att/gtatga) for

alternative 5' exon for MALAP2.03"

join(6794. :6857,6942. .7075,7272. .7383,7566. .7663,

7792. :8064,8151. :8357,8454. :8588.8638. .9609,9740. .10018,

10170. :10250.10340. .10378,10551. .10706,10776. .10787)
                                                                                                                                                                                                                                                                                                               join(6794. 6857,6942. .7075,7272. .7383,7566. .7663, 7792. .8064,8151. .8357,8454. .8588,8638. .9609,9740. .10018, 10170. .10250,10340. .10378,10551. .10706,10776. .10787) /gene="MAL4P2.03" hypothetical protein, len: 853 aa, 13 /notte-manalet some splice predictions are tentative and alternatives exist."
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   /translation="MYRNIKYFLTNWKRTYRHYSRKQNINNLSNKIKDPYSDLYKSS
MYGNNFKILDNKKTKSREYEIIKTSNNTYSYTSPYPPNINYTLTPYPESSKKMYYENR
KYIMKYKNVEYIPIKRLTYKNASKKTNWNTYYIRMEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-*hypothetical protein"
/protein_id-"CAB62844.1"
/db_xref-*C1:6562705"
/db_xref-*C2:6562705"
/db_xref-*C2:6705"
/db_xref-*C3PREMBL:QUUG9"
/translation-*MAVEDRYKLIKERYKEIKEQNDILKKAIIEYKKDLKELEKKNDI
LSNDKNQLQKNLTQLTNSLEEQKKKNSGWTNLMLLTKNSRENIHKSVAFEELEMKIKE
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MNTLHDLIVSLEKQINKINSEKNVNKFFIMCSICSNKNNIGRKYNPTCNMLYGLF"
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/note="predicted splice acceptor sequence for exon 2 of
MALAP2.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7076. .7081
/note="predicted splice donor sequence, caa/gtaaat, for exon 2 of MAL4P2.03"
7262. .7271
/note="predicted splice acceptor sequence for exon 3 of MAL4P2.03"
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/note="predicted splice acceptor sequence for exon 4 of
MAL4P2.03"
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/note="predicted splice acceptor sequence for exon 6 of
MAL4P2.03"
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//note="predicted splice donor sequence, atg/gtaata, for
exon lof MAL4P2.03"
6932. 6941
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//note-"potential splice donor sequence, atg/gtaaaa, for
exon 3 of WAL4P2.03"
7556. .7568
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/note="predicted splice donor sequence, aac/gtttgt, for
exon 4 of MAL4P2.03"
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/note="potential splice donor sequence, caa/gtaaaa, for
exon 5 of MAL4P2.03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"predicted splice acceptor sequence for exon 5 of
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9519 9618: gap of 15188: cont.g of 2510 bp 2... 13289 13388: gap of 100 bp 13389 15599: cont.g of 2211 bp in length 15600 15699: gap of 100 bp 15700 21304: cont.g of 5605 bp in length 21305 21404: gap of 100 bp 21405 26070: cont.g of 4666 bp in length 26070: gap of 100 bp 26071 26170: gap of 100 bp 26071 
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* 91606 101191: contig of 9586 bp in length

* 101192 101291: gap of 100 bp

* 101192 101391: gap of 100 bp

* 101292 110389: contig of 9088 bp in length

* 101390 110489: gap of 100 bp

* 120868 120867: gap of 100 bp
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43487: contig of 5363 bp in length
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All repeats were identified using Repeathasker:

Center Whitehead Institute/ MIT Center for Genome Center

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Center sequence submissions@genome.wi.mit.edu

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Center project name: L88, D., 1
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1 (bases 1 to 144457)
1 Elsran, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 9, clone RP11-168021
                                                                     clone RP11-168D21 map 9, WORKING DRAFT
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Insert size: 142357; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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                                                                Homo sapiens chromosome 9 clon
SEQUENCE, 22 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                  144457 bp
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DEFINITION
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Maximum Match 100%
Listing first 45 summaries
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em_gss_humg: em_gss_inv1: em_gss_inv2: em_gss_inv3: em_gss_other: em_gss_pln1: em_gss_pln1: em_gss_pln2:*

em_gss_rod1: *
em_gss_rod2: *
em_gss_rod3: *
em_gss_rod4: *
em_gss_rod5: *
em_gss_rot1: *
em_gss_vvt1: *
em_gss_vvt2: *
em_gss_vvt2: *

9b-9ss2: 9b-9ss3: 9b-9ss6: 9b-9ss6: 9b-9ss6: 9b-9ss7:

gb_est110:*
gb_est111:*
gb_htc:*
em_gss_fun:*
em_gss_hum1:*
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gb_gss29: gb_gss30: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_rod6:*
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nallenged w	For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seq primer: M13F-R FEATURES 107630-1001/0ualifiers	/organism="Solanum tuberosum" /cultivar="Kennebec" /db_xref="texon:4113" /clone="BPLI10Al4" /clone="BPLI10Al4"	/tissue_rype="leaf" //dev_stage="6 week old" /lab_host="6 week old" //note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: //note="Vector: pBluescript SK(-); Site_1: BtoRI; Site_2: //note="Vector: pBluescript SK(-); Site_1: Site_2: //note="Vector: pBluescript SK(-); Lise_1: EcoRI; Site_1: Site_2: //note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_1: EcoRI; Site_1: Site_2: Site_2: Site_2: Site_3:		Query Match Best Local Similarity 52.6%; Pred. No. 8.8e-27; Matches 382; Conservative 0; Mismatches 333; Indels 11; Gaps 3; Qy 78 GAGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAG 137	35 138 95	QY 198 AATCTTAAGGCCTCTTGTCTCACTCTAAAACACTACGCTTAGCGGAAATTTG 257	Qy 318 TCGADAACTTTGATCCTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAA 377	QY 378 CTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACC 437	QY 498 GGCATAGCCGTGGCTCTGACGCACATCATTGCAGATGCTAAAAGTTTTGTAATG 557 DD 446 GGTGTATCCATTGGTTTCACTAACCATGTTGGTGATGGAGCTACCATAGTAGGG 505 QY 558 TTCATCAATGCTTGGCCTATTAACAAATTAGGGAAGCGGGGACTTGTTGCCGGG 617 DD 506 TTCATTAAGGGTGGGCTCCTACTCCATAAATTCGGTGGAGATGAACAATTCTTATCGAAT 565
SUMMARIES Result Query No. Score Match Length DB ID Description	141.2 8.3 763 155 BG591758 BG591758 141 8.3 575 142 BE920468 BE920466 BE920466 127 7.5 690 155 BG599447	121 7.1 574 142 BE522746 BE522746 119.6 7.0 564 142 BE522746 BE522746 111.4 6.5 508 173 BC097054 BC097054 111.4 6.5 578 143 BF051101 BF051101 109.8 6.4 606 113 AW221049 AW221045	107.6 6.3 5/0 118 AW616119 BE242784 BE242784 107.6 6.3 5/0 118 AW616119 AK616119 AK616119 BC4361819 BC4361	18 91.6 5.4 404 121 AM737239 AM737239 EST3289104 C 19 91.6 5.4 543 119 AW650650 AW650650 EST329104 AW650650 EST329104 C 19 91.6 5.4 543 119 AW650280 AW650280 EST329104 AW650280 EST329104 C 22 87.4 5.2 783 155 BG584708 BG584708 EST486469 BG584708 EST486469 BE922378 EST426147 C 23 86.6 5.1 414 142 BE922378 BE921952 EST425721 C 24 85.4 5.0 705 114 AW299055 AW299055 EST36581 C 25 84.6 5.0 705 114 AW299055 BE187619 EST335180	84 4.9 411 142 BE921804 BE921804 82.8 4.9 487 118 AW616206 AW616206 81.4 4.8 368 142 BE9211953 BE921953 80.2 4.7 403 143 BF053202 BF053202 78.4 4.6 648 154 BG457806 BG457806 76.6 4.5 386 173 BG097680 BG097680	75.8 4.5 451 167 BE433920 BE433920 75.6 4.4 505 154 BG508632 BG508632 75.2 4.4 708 138 BE660849 BG50849 74.6 4.4 605 30 AV440958 AV440958 74.2 4.4 550 105 AL380276 AL380276 74.3 48.2 14.4 BF096979 BF096979	73.8 4.3 468 167 BE461227 BE461227 73 4.3 403 143 BF05.576 BF05.576 70.2 4.1 485 105 AL386583 BE905.576 69.8 4.1 468 142 BE902022 BE90022 69.2 4.1 569 119 AW719572 AW719572 68 4.0 561 121 AW831571 AW831571		MESOLT 1 MESOLT 12-APR-2001 DEFINITION EST499600 P. infestans-challenged leaf Solanum tuberosum cDNA clone BPLI10A14 5' sequence. mRNA sequence. ACCESSION BG591758.1 GI:13609898 KEYWORDS EST. COURTED COUR	ORGANISM Solanum tuberosum ORGANISM Solanum tuberosum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta: eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. REFERENCE 1 (bases 1 to 763) AUTHORS Zhang, P., Hernandez, M., Tornqvist, CE, Wirtz, U., Loukoianov, A., Rangel, P., Haberlach, G.T., Cho, J., Chlemingo, A., Bougri, O., Buell , C.R., Ronning, C.M., Helgeson, J. and Baker, B.

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123 ATGTGCTGGAGATTTTAGAGCACGATTCAATCCACCACTCCTCAATCTTTTGGGAA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sateridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 575)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning Generation of ESTs from potato leaves and petioles
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                        BE920468 575 bp mRNA EST 02-0CT-2000 ST1412137 potato leaves and petioles Solanum tuberosum cDNA clone CSTB6C8 5' sequence, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                      737
                                                                                                                                                              677
                                                                                                                                          CGATTCAACAAGGTACGAGCTACATATGTCCTCCCTTGCTGAAATCCAGAAGCTAAAG 797
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                    618 AATCTTCCATCTTCGATAGATCGATAATCAAAGATCTGTATGGCCTAGAGGAAACA
                                                                     TTTTGGAACGAAATGCAAGATGTTCTTGAAATGTTCTCTAGATTTGGAAGCAAACCCCCT
                                                                                         21;
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/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
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0; Mismatches 215;
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58.4%; Pred. No. 9.2e-27
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/cultivar="Kennebec"
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/clone="cSTB6C8"
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/note="Vector: DBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers: The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were forced in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    potato.
Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 690)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C. R., Ronning, C., Tanksley, S. and Baker, B.
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG599447 690 bp mRNA EST 12-APR-2001
EST504342 cSTS Solanum tuberosum cDNA clone cSTS25122 5' sequence,
                                                                                                                   1070 GCTTCTTGTTGCAGTTGCAGCTATTGGAGAGCCATTGAAAAGAGGTTGCACAACGAAAA 1129
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                         303 ATGGGTCCTTAATGGTG-----ATTGGTTAAAAGAGTTGGACAACGTAGACTTAATTCG
                                                                                                                                                                                                                                                                                                                                                                                                    1013 CTGTCTTGCGTCATGCGTTGCAAAAGCAACA---CATAAAGAGTTAGTTGGGGATAAAGG
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/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="GSTS5122"
/clone_lib="cSTS"
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tomato fruit tissue,
Generation of ESTs from tomato fruit tiss Unpublished (2000)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
IOU Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum
Sukaryota: Vifidiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 bp mRNA EST 24-JUL-2000 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
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                                                                          AATGCCAAGTTACACCACCATCTGACACAAGATGTCGAGTTATCGCTACCGGTAACAT
                                                                                         4 AATGTCAAGTTGCGCCACCTCCGGGGGGGA---GCGGAGGTGAACTTCCCTCTTACTT
                                                                                                                                   TCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTCTGTTTTACGACTTTC
                                                                                                                                                                 61 ATTTTGATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGATATTATTCTACAAGCTCC
                                                                                                                                                                                                               GATATCCTGAGTTACATTA - - - - TGTGACAGGAGATTCTGTATCTGTTATCTG
                                                                                                                                                                                                                                                                                                                                                                           AGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAACTGGTAGATTCCAATGATTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       592 GGGTCCGTAGTAAAAGACCCATATGGACAAGGGATGTTCATATGGGAAGAAATGAAGAAA
                                                                                                                                                                                            CGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTAATCTTAAGGCCTCTTTGTCTC
                                                                                                                                                                                                                                                       TCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGCCGATCAAATCGGGCG
                                                                                                                                                                                                                                                                                                                  AAATGCCGAAGTTTCAGTACTCCCGTGATGAGGCCGACTCGATAACTTTGATCGTTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACCATGCAAGACTATAAAGTGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AT - - - CACTTTGTTCCTACGTTAGGGAACCTAAGGATGCACCCGGGGGTCCAATTAGCTC
                 Length 690;
                 7.5%; Score 127; DB 155;
llarity 52.9%; Pred. No. 5.1e-23;
Conservative 0; Mismatches 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTCTTGAAATGTTCTCTAGATTTGGAAGCAAACCCC 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST405335 tomato breaker fruit
clone cLEG15H6, mRNA sequence.
BE434257
BE434257.1 GI:9432100
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                             al Similarity
369; Conserv
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                 Query Match
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                                           Matches
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/lab_host="SolR"
/note="Vector: pBluescriptsKmCUadapt; Site_1: EcoR1;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCAACTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 ATGCAGTCCCTTCTGTTTTACGACTTTCGGTACCCAAGAACACATTTCTTGGACACTGTT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTTGTTGATGCCGATCAMATCGGGCGAAATGCCGAAGTTTCAGTACTCCGTGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCGTGGCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTT
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llarity 53.7%; Pred. No. 6.5e-22;
Conservative 0; Mismatches 252; Indels 9;
                                                                                                                                                                                                                                                       fruit, TIGR'
                                                                                                                                                           /organism="Lycopersicon esculentum"
/cultivar="Ar496"
/db_xref="taxon:4081"
/clone="cLEG15H6"
/clone="comato breaker fruit, TIG
/tissue_type="Pericarp"
/dev_stage="Peraker"
USA
                                                                                                               Location/Qualifiers
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                                                                   Email: dfrisch@Cl.EMSON.EDU
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                          BE922746 574 bp mRNA EST 02-OCT-2000 EST426515 potato leaves and petioles Solanum tuberosum cDNA clone cSTB21L12 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2
                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AGATGCAGTCCCTTCTGTTTTACGACTTTCCGTACCCCAAGAACACATTTCTTGGACACTG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 TTATCCCTAATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAATTTGTTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 GCAACATTGCTTGTCCACTAAATTCGAGTGGTTATCCTGAGTTGCGTTA-----TGTGA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 AGGGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 GTCATCAACTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 TAAGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTC 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 -TAAGGATGCACCGGGGTCAAACTAGTCCCGGTCTTAGCCATTCAAGTGACACTTTTTC 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 CTGGAGATTCTATATCTGTTACTTTTATTGAGACTGATATGAATTTCAATCATCTCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 250; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 121; DB 142;
Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB21112"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liquid nitrogen.
123 c 106
                                                                                             BE922746.1 GI:10448822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 303; Conservative
                                                                                                                                             Solanum tuberosum
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                                                                                                                              potato.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 564)

van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tankaley, S.D. and Baker, B.

Generation of ESTS from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE921494 564 bp mRNA EST 02-OCT-2000
EST425179 potato leaves and petioles Solanum tuberosum cDNA clone
cSTB13B18 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                                                                                                      490 CTAACCGTGGCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 TAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTCTGTTTTACG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 TAACTTATTTTGATCATATATGGTTCGGTTTTGGCTATATGCGTCGGATTTTATTCTACA 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 ITGAAAAATGCCAAGTTACACCACCATCTGACAACAAGATGTCGGATTATCGCTACCGG 93
                                610 TGTCCGCGAATCTTCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTATGGCCTAG
                                                                                                                                                                                                                                                                                   23 TTGAGCAATGCCAAGTTGCGCCACCTCCCCACGGCGCGCAACAGAGCTAACGCTCCCTC
                                                                                                                      550 TTGTAATGTTCATCAATGCTTGGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGT
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/clone=lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.0%; Score 119.6; DB 142; Lengt ilarity 53.8%; Pred. No. 4.6e-21; Conservative 0; Mismatches 244; Indels
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Lycopersicon.
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Best Local Simi
Matches 276;
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/cultivar="Kennebec"
/dultivar="Examon:4113"
/clone="csrafe"=taxon:4113"
/clone="csrafe"="Solato leaves and petioles"
/clone=lib="potato leaves and petioles"
/clone=lib="potato leaves and petioles"
/clone=lip="potato leaves and petioles"
/dev_stage="8 weeks old plants"
/lab_host="Sola"
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/lab_host="Sola"
/lab_host="Solated from 8 week old greenhouse grown plants. The plants were watered and fertillized freely. The tissue was immediately frozen in
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Solanum tuberosum
Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
I (bases I to 508)
Van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning
C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG097054 508 bp mRNA EST 29-JAN-2001
EST461573 potato leaves and petioles Solanum tuberosum cDNA clone
CSTB45P9 5' sequence, mRNA sequence.
                                                                                                                                  143 AGCTACCAATTTCCAAACTCGATTTGTTCAAACCATTATTCCTACTCTTAAACATTCAC 202
                                                                                                               CGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACTCGATAACTTTGATCG 3333
                                                                                                                                                                                                   453
                                                                                                                                                                                                                                                                                                                                                                                      573
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                              203 TCTCCCTCACTCTCAAACACTACACACCCTTAGCTGGCAACATTGCTTGTCCACTAAATT
                                                                                                                                                                               TTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAACTGGTAGATTCCAATG
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                                                                                                                                                                                                                                                                                                                  TGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGTGGCATAGCCGTGGCTC
                                                                                                                                                                                                                                                                                                                                     514 TGACGCCACATCATTCAATTGCAGATGCTAAAAGTTTTGTAATGTTCATCAATGCTTGGG
                                                TGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGCCGATCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
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130 c 87
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| S51 GTTTACTCAACAAA 564
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Alcala,J., Vrebblov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,R.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                      396 TIGCAIGGCCTITITIATGITATGCCACGGGTTATAAGGACCAIGCAAGACTATAAAGIG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 TTTTATCCCTTCATTCCTCAATTGGCACAACCTAAGGATGCACCGGGGGTC---AAACTA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 TTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTAATCTTAAGGCCTCTTTG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 GGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGCCGACTCGATAACTTTGATCGTT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AGTGGTTATCCTGAGTTGCGTTA-----TGTGACTGGAGATTCTATATCTGTTACTTT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 GCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAACTGGTAGATTCCAATGAT 395
                                                                                                                                                                                                                                                                 96 ACATICITCGATATCCCCIGGTTGCACTTGAATAAGATGCAGTCCCTTCTGTTTTACGAC 155
                                                                                                                                                                                                                                                                                                                               62 ACTTATTTTGATCATATNIGGTTCGGTTTTGGCTATATGCGTCGGATTTTATTCTACAAG 121
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF051101 578 bp mRNA EST 16-OCT-2000 ES7436276 tomato developing/immature green fruit Lycopersicon esculentum cDNA clone cLEM21H7 5' sequence, mRNA sequence. BF051101 GI:10804997
                                                                                                                                  36 GAAAAATGCCAAGTTACACCACCATCTGACACAACAGATGTCGAGTTATCGCTACCGGTA 95
                                                                                                                                                                                         2 GAGCAATGCCAAGTTGCGCCACCTCCCCACGGCGCGCCAACAGAGCTAACGCTCCTCTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation of ESTs from tomato fruit tissue, immature green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 TCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGCCGATCAAATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 ATTGAGACTGATATGAATTTCAATCATCTCATTGGTAACCATCCTCGAAATGCTAAGGAT
      Length 508;
                                                                        Indels
      DB 173;
6.5%; Score 111.4; DB 173 ilarity 54.0%; Pred. No. 6.8e-19; Conservative 0; Mismatches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 ACGCACATCATTCAATTCCAGATGCTAAAA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 AGTAACCATCATGTCGCTTGTGATGGAAATA 503
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Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@cLemSoN.EDU.
Location/Qualifiers
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                                                                                                           /note="Vector: pBluescriptSKmcUadapt; Site_1: EcoR1; Site_2: Xhol; Fruit were tagged at 5 dpa (0.5 cm) and harvested at 7 day intervals through 35 dpa. Equal masses of tissue from each stage were combined (including seeds and locules) prior to mRNA isolation."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW221049 606 bp mRNA EST 07-DEC-1999 EST297518 tomato fruit mature green, TAMU Lycopersicon esculentum CADA clone cLEF3F1, mRNA sequence. AW221049 GI:6532733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTCTTGCGTCATGCGTTGCAAAAGCAACA---CATAAAGAGTTAGTTGGGGGATAAAGGG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITACAGCGGATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAAC 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --AGAGGACGCATAGGAGAAGAGATCATAGATCATAGTGTAATGGAATGTTTCGGA 418
                                                                     /tissue_type="fruit"
/dev_stage="immature green (5-35 days post-anthesis)"
/lab_host="SoLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAAACCCCCTCGATTCAACAAGGTACGAGCTACATATGTCCTCTCCCTTGCTGAAATC 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           953
                                                                                                                                                                                                                                                                                           546 AGTITIGIAATGITCATCATGCTTGGGCCTATATTAACAAATTTGGGAAAGACGCGGAC 605
                                                                                                                                                                                                                                                                                                                                                                  CTAGAGGAAACATTTTGGAACGAAATGCAAGATGTTCTTGAAATGTTCTTGGA 725
                                                                                                                                                                                                                                                                                                                                                    TTGTTGTTCCGCGAATCTTCCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTATGGC 665
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                        64
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/b_xref="cultivar="0.401"
/clone="c.EEM2147"
/clone_lib="tomato developing/immature green fruit"
                                                                                                                                                                                                                                                                                                                                                                                                                          242 GAGAAACTGAAGAATTTTATATTGAACTCAAGAAGACGGGGTAGTAGTAGTACTACTCTA
                                                                                                                                                                                                                                                                                                                       5 ACTATAGCAGGGTTCATTAAGGCGTGGGCTCTACTCCACAAATTCGGTGGACATGAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGAAGCTAAAGAACAAAGTACTGAATCTCAGAGGATCCG------AACCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           834 ATACGTGTAACGACGTTCACAATGACGTGTGGATACGTATGGACATGCTCAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                894 AAAGATGACGTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                     Score 111.4; DB 143; Length
Pred. No. 7e-19;
0; Mismatches 241; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.5%;
                                                                                                                                                                                                                                                                Matches 317; Conservative
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                192
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                                                                                                                                                                              BASE COUNT
ORIGIN
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Alcala, J. Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Opton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato fruit tissue Unpublished (1999)

Contact: David Frisch
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; cLEF - Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seeds and locules were discarded prior to freezing the pericarp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 CCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 TGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAAC 378
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .606 | Continue | C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 Jordan Hall, Člemson, s
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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1. (bases 1 to 603)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D. Generation of ESTs from wild tomato (Lycopersicon hirsutum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon hirsutum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded mixture of cells which is highly enriched for trichome likely with minor contaminations of other types of leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 24-MAR-2000
Cornell University Lycopersicon
mRNA sequence.
                                                                                                                                                                                                                                412
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/db_xref="taxon:62890"
/clone=lib="L. hirsutum trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
 299 ---TGTGACAGGAGATTCTGTATCTGTTACTTTTTCTGAGACTGATATGGATTTCAATTA
                                                                                                                                                                                                                 356 TCTCATTGGTGACCATCCGCGTAATGCTAAGGATTTTTAT---CACTTTGTTCCTACGTT
                                                                                                                                                                                                                                                                                                                                                             242 GCTTAGCGGAAATTTGTTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTC
                                                                                                                         302 CCGTGATGAGGGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTA
                                                                                                                                                                                                 362 CCTTAAAGGTCATCAACIGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCC
                                                                                                                                                                                                                                                                                       482 CGTTTTTCCTAACCGTGGCATAGCCGTGGCTCTGACGCACATCATTCAATTGCAGATGC
                                                                                      242 CTTAGCTGGAAACGTTGCTCGTCCACTAGATACAAACGGATATCCTGAGTTACATTA---
                                                                                                                                                                                                                                                                     422 ACGGGTTATAAGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon hirsutum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: David Frisch
Contact: David Frisch
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                               574
                                                                                                                                                                                                                                                                                                                                                                                                                                 533 AGCTACCATAGTAGGGGTTCATTAGGGCGTGGGC 565
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EST296884 L. hirsutum trichome,
hirsutum cDNA clone cLHT6C7 3',
AW616119
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1. .603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prime sequence.
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ORIGIN
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AW616119/C
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DEFINITION
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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                                                                                                                                                                                                                                                                                     potato leaves and petioles Solanum tuberosum cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 TGACACAACAGATGTCGAGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGGTTGCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCATCAATGCTTGGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGTTGTCCGCGA
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499 GCATAGCCGTGGCTCTGACGGCACATCCAATTGCAGATGCTAAAAGTTTTGTAATGT
                      180 t
                                                                                                                                                                                                                                                                                  EST426553 potato leaves and petioles
CSTB32E2 5' sequence, mRNA sequence.
BE922784.1 GI:10448860
                                                                                                                                                                                                                                                                     HRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liquid nitrogen
                                                                                                                                                                                                                                                                   570 bp
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                                                                                                                                         619 ATCTTCTTCCATCTT 633
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                                                                                                                                                                                                                                                                                                                                                                            potato.
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                                                                    559
                                                                                                                                                                                                                                RESULT 10
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AUTHORS
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JOURNAL
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Seg primer: M13F-R.
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                                                                                                                     COUNT
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JOURNAL
COMMENT
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BG598154
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                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 542)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 24-JUL-2000
TIGR Lycopersicon esculentum cDNA
                                                                                                                                                                                                                                    1199
                                                                                                                                                                                                                                                                                                                                                    1260 AAATTTGACATTACCTC-----TGTTGATTATGCAGAATTGATTTATGTGATTCAG 1310
                                                                                                                                                                                                                                                                                                                                                                                                            TCCAGGGATTTTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAAGATTCATATGGAT 1370
                                                          GATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCG 1022
                                                                                                                  1023 TCATGCGTTGCAAAAGCAACA---CATAAAGAGTTAGTTGGGGGATAAAGGGCTTCTTGTT 1079
                                                                                                                                                                                                       423
                                                                                                                                                                                                                                                                                          1200 ATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCA 1259
                                                                                                                                                                                                                                                                                                                                                                                249
                                                                                                                                                                                                                                                    422 AATGGTG-----ATTGGTTAAAAGTATTAGACAACATAGATGTGATTGGTTGTTTTCA 369
                                                                                                                                                 483
                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGTTGCAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTT
                                                                                                                                                                                                                                  1140 GCAGATGCAAAAACTTGGTTATCGGAATCTAATGGAATCCCTTCAAAAAGATTTCTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation of ESTs from tomato fruit tissue, breaker stage
   Length 603;
                               18;
             .3e-18;
nes 179; Indels
   DB 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATTIGCAAAAATCTIIGAAGAAGGCTIITGCTCTIIGT 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Trel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
Score 107.6; I
Pred. No. 7.3e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE436185 542 bp mRNA
ESY407263 tomato breaker fruit,
clone cLEG31A19, mRNA sequence.
BE436185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref-"taxon:4081"
/clone-"cLEG31A19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE436185.1 GI:9434028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: David Frisch
6.3%;
ilarity 57.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prime sequence.
                Similarity
                              263;
   Query Match
                   Local
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DEFINITION
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EST496832 cSTS Solanum tuberosum cDNA clone cSTS20M23 5' sequence,
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
                                                                                                                          /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

70 c 132 g 165 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              953 TITTACAGCGGATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1013 CTGTCTTGCGTCATGCGTTGCAAAAGCAACA---CATAAAGGTTAGTTGGGGATAAAGG 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTTCTTGTTGCAGTTGCAGCTATTGGAGAGCCATTGAAAAGAGGTTGCACAACGAAAA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGCGTTCTTGCAGATGCAAAAACTTGGTTATCGGAATCTAATGGAATCCCTTCAAAAG 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTCTCGGGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGG 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 ATGTGCAGCAGATTTTAGAGCGCGATTCAATCCACCTTCCTCAATCTTATTTTGGGAA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   893 AAAAGATGACGTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAG 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AGAGGACGCGATAGGAGAGAGATGATCATAGATGATAGTGTAATGGAATGTTTCGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCATTTTCAATTGCTGGATCGCAAAAACATGACTTATATGCTGCTGATTTTGGATGGGG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chiemingo, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 AACTCATGTAACATCTTTTACTGTAACGAGTGCTTATATATGGACTTGTTTGATAAAATC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Gaps
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the Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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1 (bases 1 to 659)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of Esrs from sprouting potato eyes
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 ATGGGTCCTTAATGGTG-----ATTGGTTAAAAGTATACGACAATGTAGATGTGATTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 107.2; DB 167; Lengt
Pred. No. 9e-18;
0; Mismatches 188; Indels
/clone_lib="tomato breaker fruit, TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1250 AAAGCCTGCAAAATTTGACATTACCTCTGTTGATTATGCAGA 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              479 AAGAGCCGCAAAGTTGGAATTCATTTCCATTGACAATGATGA 520
                                  /tissue_type="Pericarp"
                                                              /dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG598154.1 GI:13616294
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Matches 262; Conservative
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BG598154
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us-08-894-356c-1.rst

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l (bases 1 to 497)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannon1,J. Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: David Frisch
                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; CLSF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verlify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 TCTTTGTCTCTCACTCTAANACACTACGTTCCGCTTAGCGGAAATTTGTTGTTGTGCGATC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GATACAAACGGATATCCTGAGTTACGTTA-----TGTGACAGAGATTCTGTGTGTTT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 ACTITITICGAGACTGATANGAATTTCAATTATCTCATTGGTGACCATCCGCGTAAGGCT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 AATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACCATGCAAGACTAT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 GGTTTCACTAACCATCATGTTGTTGTTGATGGAGCTACTATAGCAGGTTCATTAAGGG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 AAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACTCGATAACTTTG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 ATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAACTGGTAGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="fruit pericarp" //dev_stage="mature green (3-5 days pre-ripening)" /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             570 TGGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGTTGTCCGCGGAATCTTCTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 GCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTTGTAATGTTCATCAATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 TGGGCTCTACTCCACAAATTCGGTGGACATGAACAATTCTTATCGAATGAGCTAATTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 6.0%; Score 101.6; DB 122; Length 497; Best Local Similarity 54.0%; Pred. No. 2.7e-16; Matches 256; Conservative 0; Mismatches 209; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .497
/organism="Lycopersicon esculentum"
/cultivar="May96"
/cultivar="Tay96"
/clone="cLEF42M23"
/clone=lib="comato fruit mature green, TAMU"
                                                                                                                                                                                                                                                                                                                                 100 Jordan Hall, Člemson, SC 29634, USA Tel: 864 656 4293 Fex: 864 656 4293 Emall: dfrisch@cLEMSON.EDU
                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute
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                                                                                                                                                                                                                    /note-"vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 TTGAGCAATGCCAAGTTGCGCCACCTCCCCACGGCGGCGCAACAGAGCTAACGCTCCCTC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 TAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTCTGTTTTACG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTACCAATTTCCAAACTCGATTTCGTTCAAACCATTATTCCTACTCTTAAACATTCAC 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTITIATCCCTTCATTCCTCAATTGCCACAACCTAAGGATGCACCGGGGGTC---AAAC 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 102.8; DB 155; Length 659;
Pred. No. 1.4e-16;
0; Mismatches 257; Indels 13; ¿Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 TTGAAAAATGCCAAGTTACACCACCATCTGACACAACAGATGTCGAGTTATCGCTACCGG
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                                                                                                   /clone_lib="cSTS20N23"
/clone_lib="cSTS"
/tissue_kype="sprouting eyes from tubers"
/dev_stage="l2-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571 GGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGTT 610
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                                              /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                          206
                                                                /cultivar="Kennebec"
/db_xref="taxon:4113"
Location/Qualifiers
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Best Local Similarity 53.4%;
Matches 310; Conservative (
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of ESTs from tomato fruit tissue
Contact: David Frisch
                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Xhol: cLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to rippening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                        AW221050 583 bp mRNA EST 07-DEC-1999
EST297519 tomato fruit mature green, TAMU Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 GGATATTATTACAAGGTCTCCATTTTCAAACCCGATTTCGTTCAAAACATTATTCCTC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 TGATGCCGATCAAATCGGCCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGGCT 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ACATGGCCACCGTGATTGAGCAATGTCAAGTTGCGCCACCTCCCGGCGCGCAACGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
Score 101; DB 113; Length 583;
Pred. No. 4.1e-16;
0; Mismatches 260; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .583
/organism="Lycopersicon esculentum"
/cultivar="Ty496"
/cultivar="Ty496"
/clone="CLEF3F3"
/clone=lib='tomato fruit mature green, TAMU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
184 656 436
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                         CDNA clone cLEF3F3, mRNA sequence.
AW221050
AW221050.1 GI:6532734
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                                                                                                                                                                                                                                 Lycopersicon esculentum
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Matches 299; Conservative
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AW221050
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JOURNAL
COMMENT
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Sequence 35,
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APPLICANT: Takeshita, Makoto
APPLICANT: Rawai, Shinji
APPLICANT: Rawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Tsujimura, Asushi
APPLICANT: Tsujimura, Asushi
APPLICANT: Tsujimura, Asushi
APPLICANT: Manni, Bono-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF MEK1 EXPRESSION
FILE REPERENCE: RTS-0016
CURRENT APPLICATION NUMBER: US/09/197,380
CURRENT FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 47
LENGTH: 2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.8; DB 3; Length 2:
Pred. No. 0.022;
` '''smatches 37; Indels
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US-09-031-485-3

US-08-847-429A-1

US-08-847-429A-3

US-09-065-474-3

US-09-031-485-6

US-09-031-485-6

US-08-847-429A-6

US-08-847-429A-6

US-09-065-474-6

US-09-065-474-6

US-09-065-474-8

US-09-065-474-8

US-09-031-485-35

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; Sequence 1, Application US/03738349
; Patent No. 5869538
; GENERAL INFORMATION:
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Best Local Similarity 63.4%;
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US-09-197-380-1
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US-09-197-380-1
       DNA
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                                                                                                                                                                                                                                                                                                            Sequence 144,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64, 1
Sequence 10, 1
Sequence 102,
                                                                                                                                                                      ; Search time 168.74 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, A Sequence 9, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 146,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, 1
Sequence 5, 1
Sequence 4, 1
Sequence 5, 1
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Sequence 2,
Sequence 9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ogn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-684-862-10
US-09-065-474-102
US-09-065-474-103
US-09-031-485-9
US-09-031-485-10
US-08-847-429A-9
US-08-847-429A-10
US-08-847-429A-10
US-08-065-474-9
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US-09-065-474-146
US-09-031-485-4
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-08-684-862-10
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US-08-021-608D-9
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US-08-821-994-64
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US-09-065-474-5
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US-08-726-160-1
                                                                                                                                                                                                                                                                                                                                                                                                                               324599 seqs, 94655562 residues
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                                                                                                                                                                   5, 2001, 13:53:20
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1703
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Match Length
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1616 ATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATG 1675
                                                                                                                         7003 acattatacttttataactaatagataacagttttttacatattaaatatgttctacttaa 7062
                                                                                             1585 ACCTCACACCTGACATGGTGTTACGATAGGTATTGTATAATGCCATTATATACTTCCATA 1644
                                                                                                                                                                               Query Match 2.3%; Score 38.4; DB 1; Length 2381; Best Local Similarity 64.8%; Pred. No. 0.22; Matches 57; Conservative 0; Mismatches 31; Indels 0
              DB 4; Length 7122,
                                                       Indels
                                                     50;
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                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
            2.3%; Score 39; DB 4; 58.0%; Pred. No. 0.24;
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S FEILER
REGIGENATION NUMBER: 2026-4063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08021608D Patent No. 5580760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: MORGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
Query Match
Best Local Similarity 58.0%
".....hrhes 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2.
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
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COTHER INFORMATION:
US-08-021-608D-9
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: YES ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                  US-08-021-608D-9
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US-09-318-448-2
US-09-318-448-2
Sequence 2, Application US/09318448
Fatent No. 6210950
GENRRAL INFORMATION:
APPLICANT: Johnson, William G.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 7122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-CT-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE: 26-AUG-1993
ATYONEY/AGENT INFORMATION:
NAME: BARKET INFORMATION:
NAME: BARKET N. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELEPHONE: 202-408-4000
TELEFMX: 202-408-4000
TATABWARTION FOR SET IN NO. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.3%; Score 39.8; DB 2;
1larity 79.7%; Pred. No. 0.1;
Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
STRAIN: osteoblastic cell line MC3T3E1
                             : 1300 I Street, N.W. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA to MRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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284..2671
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CRGANISM: Homo sapiens
US-09-318-448-2
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Best Local Similarity
              Dunner
            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
US-08-738-349-1
                                                                                             COUNTRY:
                                                     CITY:
STATE:
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Sequence 9, Application PC/TUS9401782
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38.4; DB 5;
Pred. No. 0.22;
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: TABM FO COMPATIBLE
CORNUTER: TABM FO COMPATIBLE
CORNUTER: TABM FO COMPATIBLE
CORNUTER: TABM FO COMPATIBLE
CORNUTER: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: PCT/US94/01782
FILING DATE: 22-FEB-1994
CLASSIFICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
APPLICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEBILER
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 26,738
REFERENCE/DOCKET NUMBER: 26,738
REFERENCE/COMPATION FOR SEQ 120 751-6849
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE: CHARACTERISTICS:
      2320 TCAAAAAAAAAAAAAAAAAAAAAAAAAAA 2347
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEW YORK
: USA
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ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10154
                                                                                                  RESULT 6
PCT-US94-01782-9
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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2260 AATGTATACATTTCACATTCCAAATGCCTGTTTTGTGCTTTACAATGATAAATGAAACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2260 AATGTATACTTTCACTTTCCAAATGCCTGTTTTGTGCTTTACAATAAATGATAGAAACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1616 ATTGTATAATGCCATTATATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATG 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%; Score 38.4; DB 1; Length 2381; 64.8%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08726160
Patent No. 5734016
GENERAL INFORMATION
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 bp variable region where R is A or G.
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CALLY
CALLY
CALLY
MEDIUM TYPE: FLOPPY DISK
COMPUTER: TBM FO COMPATIBLE
COMPUTER: TBM FO COMPATIBLE
COPERATING
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDFERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-OCT-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,608
FILING DATE: 22-FEB-1993
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 2026-4063US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 759-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEMENTICE
CONTAINS
CONT
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                                                                                              1676 TGTTAAAAAAAAAAAAAAAAAAAAAAA 1703
                                                                                                                                                               2320 TCAAAAAAAAAAAAAAAAAAAAA 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.3 Best Local Similarity 64.8 Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
US-08-726-160-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2381
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Length 2381;

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2323 TCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2350
                     1676 TGTTAAAAAAAAAAAAAAAAAAAAAA 1703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,160
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-0CT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/021,608
FILING DATE: 22-FEB:1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION UNUBER: 26,728
REFERENCE/DOCKET UNUBER: 2026-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                       Sequence 1, Application US/08726160 Patent No. 5734016
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2384
TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-726-160-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                          USA
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                    10154
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                                                                                                                RESULT 8
US-08-726-160-1
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                                     1616 ATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATG 1675
                                                                          2260 AATGTATACTTTCACTTTCCAAATGCCTGTTTTGTGCTTTACAATAAATGATATGAAACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1616 ATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATG 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2263 AATGTATACTTTCACTTTCCAAATGCCTGTTTTGTGCTTTACAATAAATGATATGAAACC 2322
   0; Gaps
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 31; Indels
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variable region where R is A or G.
                                                                                                                                                                                                                                            Sequence 1. Application US/08021608D
Fatent No. 5580760
GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
TUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.3%; Score 38.4; DB 1;
64.8%; Pred. No. 0.22;
tive 0; Mismatches 31;
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DUS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATE: US/08/021,608D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FETLER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                              1676 TGTTAAAAAAAAAAAAAAAAAAAAAAA 1703
                                                                                                                                                     2320 TCAAAAAAAAAAAAAAAAAAAAAA 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                       : 345 PARK AVENUE
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.3'
Best Local Similarity 64.8'
Matches 57; Conservative
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-FEB-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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HYPOTHETICAL:
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                                                                                                                                                                                                                              US-08-021-608D-1
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 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 bp
variable region where R is A or G.
GENERAL INFORMATION:
APPLICANT: LEVENSS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVITAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2323 TCAAAAAAAAAAAAAAAAAAAAAAA 2350
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1616 ATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATG 1675
                           2263 AATGTATACTTTCCAAATGCCTGTTTGTGCTTTACAATAAATGATAGAAACC 2322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1602 GTGTTACGATAGGTATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATA 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bach, Alfred
APPLICANT: Hillen, Heinz
APPLICANT: Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kell & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 1474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage.
COMPUTER: IBM AT-compatible, 80.286 processor
OPERATING SYSTEM: MS-DOS version 5.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
PFILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%; Score 38; DB 4;
60.8%; Pred. No. 0.22;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Greenland, Andrew J
APPLICANT: Jepson, Ian
TTLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER APPLICATION NUMBER: GB 9606062.9
SOFTWARE: PLING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PALENTING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PALENTING DATE: 1496-03-22
NUMBER OF SEQ ID NOS: 89
LENGTH: 1474
                                                                                           1676 TGTTAAAAAAAAAAAAAAAAAAAAAAA 1703
                                                                                                                  RESULT 10
US-08-321.994-64
Sequence 64, Application US/08821994A
Patent No. 6228643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-08-684-862-10
'Sequence 10, Application US/08684862;
Patent No. 5759541
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Brassica napus
US-08-821-994-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
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                                                                                                        APPLICANT: THE GOVERNMENT OF THE UNITED STATES
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 473 bp
OTHER INFORMATION: variable region where R is A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-689
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2384
LENGTH: 2384
LENGTH: 2384
TYPE: NUCleic acid
STRANDEDNESS: Double
TYPE: Unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 22-FEB-1994
                                                              Sequence 1, Application PC/TUS9401782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10154
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
IDENTIFICATION METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANELLE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
              RESULT 9
PCT-US94-01782-1
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Gaps

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1042 CACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAG 1101
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                                                                                                                                                                                                                                                                                                                            26 CACAAGAACCGTTTTTCAGCAAGTAGGCTATAATGGGACACCTGGAGATCCAGAAGAAC 85
                                                                                                                                                                                                                                                                                                                                                                                        1102 CCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACTTG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                     86 CCAAAGAACAGTCCATTCCACGAAGAGGAAGTTGCAGTTTCAGAAATTCG 140
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                                                                                                                                                                                                                 DB 3; Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 103, Application US/09065474

Patent No. 6063599
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DESTRIBENCE AND TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
                                                                                                                                                                                                            Score 36.6; DB Pred. No. 0.21; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         =
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24-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 103:
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ilarity 57.4%;
Conservative 0
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LENGTH: 184 nucleotides
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Best Local Similarity 57.47
Matches 66; Conservative
         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                              TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                 NAME/KEY: CDS
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; MOLECULE TYPE:
US-09-065-474-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-065-474-103/c
                                                                                                                                           US-09-065-474-102
                                                                                                                      LOCATION:
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Patent No. 6063599

GENERAL INFORMATION:

GENERAL INFORMATION:

TAPLICANT: Blehm, E. Scot

TITLE OF INVENTION:

TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN

TITLE OF INVENTION: DROFILARIA AND BRUGIA ANKYRIN

TITLE OF INVENTION: DRES THEREOF

CORRESPONDENCES: 171

CORRESPONDENCE ADDRESS:

ADDRESSE: Garol Talkington Verser, Ph.D.

ADDRESSE: Heska Corporation

STREET: 1825 Sharp Point Drive

CIUTY: Fort Collins

STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 197 to 904

CTHER INFORMATION: the coding region shown in (2)(ix)(B)

CTHER INFORMATION: codes for the protein of SEQ ID NO: 5
US-08-684-862-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 2.2%; Score 37.2; DB 1; Length 9 Best Local Similarity 77.6%; Pred. No. 0.31; Matches 45; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect for Windows, Version 7.0 CURRENT APPLICATION DATA:
                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/966,040
FILING DATE: 30-DEC-1992
APPLICATION NUMBER: PCT/EP91/01361
FILING DATE: 19-JUL-1991
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 988 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/065,474 FILING DATE: 24-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Agkistrodon rhodostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS: LENGTH: 184 nucleotides TVPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                            CDNA to mRNA
                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line
MOLECULE TYPE: c
ORIGINAL SOURCE:
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                                                                     FILING DATE:
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Search completed: November 5, 2001, 18:03:41
Job time: 15021 sec
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159 CAÇAAGAACCGTTTTTCAGCAAGTAGGGTATAATGGGACACCTGGAGATCCAGAAGAAC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 CACAAGAACCGTTTTTCAGCAAGTAGGGTATAATGGGACACCTGGAGATCCAGAAGAAC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                           1102 CCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAACTTG 1156
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                                                                                                                                                                                                                                                                       APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DISCPLILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DISCPLILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STREET: Colorado
                                                                      Score 36.6; DB 1; Length 810;
Pred. No. 0.42;
0; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-ARR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/031,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Verser, Carol Talkington
REGISTRATION VUMBER: 37 459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           Sequence 9, Application US/09031485 Patent No. 5824306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 810 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%;
Best Local Similarity 57.4%;
Matches 66; Conservative (
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: CDN2
US-09-031-485-9
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US-09-031-485-10/c ; Sequence 10, Application US/09031485 percent No. 5824306 ; GENERAL INFORMATION:

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1042 CACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAG 1101
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  DIROFILARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES, AND
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Indels
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlsk
COMPUTER: IBM PC COMPATIALS
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
2.1%; Score 36.6; DB 1;
Best Local Similarity 57.4%; Pred. No. 0.42;
Matches 66; Conservative 0; Mismatches 49;
                                                                     NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                CURKENT AFFLICATION NUMBER: US/09/031,485
FILING DATE: CLASIPECATION: 530
CLASIPECATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 810 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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; MOLECULE TYPE:
US-09-031-485-10
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Arabidopsis thalia Human colon cancer Human MEK1 DNA. H Human breast cance

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Human Gl protein i

Perfect score:

Sequence:

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Scoring table:

Searched:

Database

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Aromatic acyl transferase: transformation; anthocyanin pigment; plants; acylation; colour: tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
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6.1415
7/ttgg - Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                  Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                              Gentiana triflora var. japonica (Clone pGAT4).
                                                                                                                                                                                                                                                                                                   Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                              AAT37308 standard; cDNA to mRNA; 1703 BP.
                               AAF58255
AAC64785
AAC46852
                                                                                                        AAC66940
AAQ44391
AAX51737
AAX33336
AAZ33336
AAF31100
AAC91207
AAA46483
                                                                                            AAF17559
AAA79685
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95JP-0067159.
95JP-0196915.
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                                                                                                                                                                                                                                                                                      (first entry)
(SUNR ) SUNTORY LTD
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17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                          WO9625500-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1996;
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AAT37308;
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Oligonucleotide D2
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2400.315 Million cell updates/sec
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                                                                 ; Search time 445.49 Seconds
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                                                                                                                                                                                       /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*
                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/geneseq/geneseqn/NA1997.
/SIDS1/gcgdata/geneseq/geneseqn/NA1998.
/SIDS1/gcgdata/geneseq/geneseqn/NA1999.
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                               730101 seqs, 313950809 residues
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                                          November 5, 2001, 13:54:25
                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
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AAT37309
AAT37311
AAF58252
AAF58254
AAF58259
AAF58259

    nucleic search, using sw model

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AAT37312
                                                                                            IDENTITY_NUC
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Maximum DB seq length: 2000000000
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Score

Result è. 1698.2 202.4 193 193 172.2 110 110 110 110 110

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Nucleotide sequenc N. tabacum TOB-F12 Rice 4-hydroxyphen Human breast and o Human c-myc far up Human c-myc far up Human Secreted pro

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n colour Six plants Vectors containing DNA fragments encoding proteins of plant originate aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colotone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313. DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers Ξ Mizutani Ė Kusumi 94pp; Japanese Υ, Fukui ľ, Fujiwara H, Fuk Tanaka Y, Yonekura 53-57; 1996-393401/39 P-PSDB; AAW04722 Page Ashikari Nakao M, Claim 4; NAME OF COLORS OF STREET AND C

T; 0 other; G; 482 BP; 512 A; 353 C; 356 Sequence 1703

ö 180 180 240 300 300 360 360 420 420 480 480 540 120 540 900 99 999 9 9 TCATTATGGAGCAAATCCAAATGGTGAAGGTTCTTGAAAAATGCCAAGTTACACCACCAT CTGACACACAGATGTCGAGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGGTTGC TGGACACTGTTATCCCTAATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTC CCCGTGATGAGGGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACT ACCTTAAAAGGTCATCAACTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGC CACGGGTTATAAGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAA **ACTTGAATAAGATGCAGTCCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCT** CGCTTAGCGGAAATTTGTTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACT CTAAAAGTTTTGTAATGTTCATCAATGCTTGGGCCTATATTAACAAATTTGGGAAAGACG ctaaaaagttttgtaatgttcatcaatgcttgggcctatattaacaaatttgggaaagacg CGGACTTGTTGTCCGCGAATCTTCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGT Length 1703; ö Indels DB 17; ., ض 99.7%; Score 1698.2; llarity 99.8%; Pred. No. 0; Conservative 0; Mismatches Query Match Best Local Similarity Matches 1700; Conserv 541 121 241 361 481 61 61 121 181 181 241 301 301 361 421 421 481 601 g ag Sy 8 g ò 9 õ g S G à ò ç Q ò Op g 8 ò ò

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Scenecio cruentus; Lavandula angustifolia; ds.
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            AGATTGGAGTATCATTGCCTAAGATTCATATGGATGCATTTGCAAAAATCTTTGAAGAAG 1395
                        Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313. NOTE: This sequence is supposed to cross reference with the protein described in AAM04727, however there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide given in the specification and described in AAW04727 that the indexer decided not to cross reference the two.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                                                                                                       Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
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/product= Aromatic acyl transferase.
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Nakao M, Tanaka Y, Yonekura K;
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                                                                                                                                                                                                                 Aromatic acyl transferase coding sequence.
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                                                                                                                                                                                                                                                                                                 Lavandula angustifolia (Clone pLAT21)
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              1143 GATGCAAAAACTTGGTTATCGGAATCTAATGGAATCCCTTCAAAAAGATTTCTCGGGATT
                                                     actgtggagaactggccgtctgagattcgcgaagccttgcaaaactgttatttctcggtg
                                                                                                                    1263 TTTGACATTACCTCTGTTGATTATGCAGAATT --- GATTTATGTGATTCAGTCCAGGGAT
                                                                                                                                                                                                                    1203 caagagatactgtcgattgatggagagagagtttacgatgtcgttgtgtaaaccgagggat
                                                                                             ACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAA
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/transl_except= ATC encodes
1322..1324
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containing DNA fragments encoding proteins of plant origin
                                                                                                                                                                                                                                                                                                                                                      25 TGAAGGTTCTTGAAAAATGCCAAGTTACACCACCATCTGACACACAGATGTCGAGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 AAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGTGGCA
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                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                          Length 1622;
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Pred. No. 4.9e-40;
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                                                                                                                                                                                                    CAAAATTTGACA - - - TTACCTCTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCA
                         TATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTACAGCGGATT
                                         taagagagaa...ggtggaagaggataaacatgcagcaacttatgtgctttcatcaact
                                                        GCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCGTCAT
                                                                                          GCGTTGCAAAAGCAACACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTG
                                                                                                                                                          1147 CAAAAACTIGGTTATCGGAATCTA-----ATGGAATCCCTTCAAAAGATTTCTCG
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/product= Aromatic acyl transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                     Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                       plants
tone,
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                                                                                                                 DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
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Mizutani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 172.2; DB 17;
Pred. No. 2.3e-36;
0; Mismatches 668;
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Kusumi
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Υ,
Fukui
                        Tanaka Y, Yonekura K;
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Fujiwara
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Best Local Simil
Matches 701; (
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                        Vakao M,
Ashikari
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690 ttaccgacggaccgcattcgaccaccaatcaaaattaagaaattg
                                                     aag...-.ggttggattcagtccagagttccaagtttagtccatctctcatctttgta
                                                                         ATGACGTGTGGATACGTATGGACATGCATGGTCAAATCAAAAGATGACGTCGTATCAGAG
                                                                                                                               CITCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCGTCATGCGTTGCA
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                                AAGAACAAAGTACTGAATCTCAGAGGATCCGAACCGACAATACGTGTAACGACGTTCACA
                                                                                              gcgattgcagcttatatgtgggctggcataacgaaatcattcacagcagatgaag----
                                                                                                                  GAATCATCGAACGACGAAAAATGAGCTCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGA
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gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAGCCATTGAAAAGAGGTT 1117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTCATATGGATGCATTTGCAAAAATCTTTGAAGAAGGCTTTTGCTCTTTGTCATAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to a composition comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and single-nucleotide polymorphisms, e.g. for genotyping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.5%; Score 110; DB 22; Best Local Similarity 1.3%; Pred. No. 8.7e-20; Matches 8; Conservative 434; Mismatches 264;
                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 127; 159pp; English.
                                                                                           (CLIN-) CLINICAL MICRO SENSORS INC.
26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monitoring gene expression.
                                                                                                                                                                                                             WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                         single surface
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                                                                                                                                                                                         1538 ATAAATTCCAGAGGTCGAATATACACCGTTGTCCTCTGAAAAGTTGAACCTCACACCTGA 1597
                                                                                                                                                                                                                                                                                                               1598 CATGGTGTTACGATAGGTATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGC 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                              1298 ITATGTGATTCAGTCCAGGGATTTTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAA
                                                                                   1358 GATTCATATGGATGCATTTGCAAAAATCTTTGAAGAGGCTTTTGCTCTTTGTCATAGTC
                                                                                                   1418 TCTTTAATAGAACCATATTTGCTGCAATAAAGTACCAAGTCCTTTAGTAACACTACACCA
                                                                                                                                                                                                                             ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC
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17-MAR-2000; 2000US-0190259.
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gene expression; ss.
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Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           (CLIN-) CLINICAL MICRO SENSORS INC.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                             Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other
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                                                                                            (CLIN-) CLINICAL MICRO SENSORS INC.
                                26-JUL-2000; 2000WO-US20476
                                                        99US-0145695
                                                                  17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                       monitoring gene expression.
                                                                                                                                           WPI; 2001-159728/16
                                                                                                                                                                                            single surface
                                                          26-JUL-1999;
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                                                                  8; Conservative 434; Mismatches 264;
        Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                             DB 22;
                                                       Pred. No. 8.7e-20;
                                            Query Match 6.5%; Score 110;
Best Local Similarity 1.1%; Pred. No. 8.
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  Length 936;
Score 110; DB 22;
Pred. No. 8.7e-20;
                                               Mismatches
                                               Conservative 434;
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1.1%; P
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                                                                                                                                           The present invention relates to a composition comprising two nucleic
                                                         ETM; mismatch; genotyping;
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gene expression; ss.
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L.1%; Pred. No. 8.7e-20;
Ive 434; Mismatches 264; Indels
                                                       ETM; mismatch; genotyping;
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AAF58262 standard; DNA; 936
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gene expression; ss.
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                                                    Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other
                                                                             6.5%; Score 110; DB 22
llarity 1.1%; Pred. No. 8.7e-20;
Conservative 434; Mismatches 26
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Best Local Similarity
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCACAACGAAAAAGGCGTTCTTGCAGATGCAAAACTTGGTTATCGGAATCTAATGGAAT 1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 936 BP; 4 A; 1.39 C; 10 G; 7 T; 776 other;
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                                                                                                                  26-JUL-2000; 2000WO-US20476
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2000US-0190259
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WO200107665-A2
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17-MAR-2000;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
 1118 GCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACTTGGTTATCGGAATCTAATGGAAT 1177
                                                    1178 CCCTTCAAAAAGATTTCTCGGGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGA 1237
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                                                                                                                                                                                Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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17-MAR-2000; 2000US-0190259
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Best Local Similarity 0.8%; Pred. No. 6.3e-19;
Matches 6; Conservative 434; Mismatches 266; Indels
                                                                                                                             Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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illarity 0.8%; Pred. No. 6.3e-19;
Conservative 434; Mismatches 266;
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17-MAR-2000; 2000US-0190259
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24-APR-2001 (first entry)
                                    Oligonucleotide D2004
                                                                                         gene expression; ss
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                                                                                                                                                                                                                                                                                                                                                                                     1058 TGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAGCCATTGAAAAGAGGTT 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACTTGGTTATCGGAATCTAATGGAAT 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              998 TAACTACTTTGGCAACTGTCTTGCGTCATGCGTTGCAAAAGCAACACATAAAGAGTTAGT 1057
                                                                        two nucleic
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                    96
                                                                   The present invention relates to a composition comprising two nuclei acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                  CCCTTCAAAAAAATTTCTCGGGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACCTCTGTTGATTATGCAGAATTGAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCCTACTTTCGAGGCGGGAACACCACAACGAGGTTCAATCACTAGAAGGTTGTACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAAATTCCAGAGGTCGAATATACACCGTTGTCCTCTGAAAAGTTGAACCTCACACCTGA
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                                                                                                                                                                                                                                            Length 936;
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                                                                                                                                                                                             Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other
                                                                                                                                                                                                                                            6.3%; Score 106.8; DB
llarity 0.8%; Pred. No. 6.3e-19;
Conservative 434; Mismatches 26
                                  Example 6; Page 127; 159pp; English
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                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
   single surface
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Length 936;

group, useful as labels in allowing repeat analyses on

Search completed: November 5, 2001, 18:11:15 Job time: 15410 sec

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4080
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923
11736
11736
11736
8920
88920
8877
260
2230
923
923
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CITY:
STATE:
RESULT
                                                                      (without alignments)
1800.666 Million cell updates/sec
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Sequence 64, Appl
Patent No. 5198347
Sequence 10, Appl
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Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Appl
                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                         ; Search time 168.74 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, A Sequence 12, Sequence 22, Sequence 22, Sequence 2, A Sequence 2, A Sequence 1, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, P
Sequence 1, P
Sequence 1, P
Sequence 1, P
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Sequence 3, 1
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                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-545-1968-10
US-08-545-1968-12
US-09-370-253-1
US-08-361-4678-4
US-08-361-4678-4
US-08-357-762-1
US-08-326-1194-1
US-08-072-610-1
US-08-719-8228-1
US-08-719-8228-1
US-08-73-458-1
US-08-834-306-22
US-08-933-674A-22
US-08-933-674A-22
US-08-933-674A-22
US-08-933-674A-22
US-08-933-674A-22
US-08-933-674A-22
US-08-933-674A-22
US-09-013-810-1
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-557-128-12
US-08-375-300-3
US-09-177-431-3
                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-463-14
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US-08-821-994-64
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US-08-375-300-1
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                                                            November 5, 2001, 18:04:15
                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
                                                                                                                                   IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                Issued_Patents_NA:*
                                                                                                                                                                                                  Minimum DB seq length: 0 Maximum DB seq length: 20000000000
                                                                                                 US-08-894-356C-3
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                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
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40.8
40.6
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                                                                                                         Perfect score:
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                                                             Run on
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
PCT-0X55-16930-1

US-08-721-488-9

US-09-004-731-66

US-09-182-816-22

US-09-182-816-24

US-09-182-816-24

US-09-180-185-816-24

US-09-471-528-24

US-09-471-528-24

US-09-471-528-24

US-08-471-528-24

US-08-471-340-1

US-08-520-678A-29

US-08-520-678A-29

US-08-948-813-24

US-08-96-96-96-144

US-08-96-616-144
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Sequence 14, Application US/08232463

Patent No. 567036,
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: C6-MC-191
ATORNEY AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 20,768
TELEFANGE: (703)835-9300
TELEFANGE: (703)835-9300
TELEFAN: (703)835-4109
TELEFAN: (703)83-4109
TELEFAN: (703)83-4109
TELEFAN: REGISTRATION NUMBER: SEGUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-012-431-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Laröner
STREET: 1800 Diagonal Foad, Suite 500
CITY: Alexandria
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CLONE:
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                                                                                                                                                           1044 TTTGTTACTAGCAAGCCCGATCGAGTTCGCTGGTGGGATGATACAACAAGCGATCGTGAA 1103
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                                                                                       Gaps
Query Match 4.2%; Score 67; DB 1; Length 7218; Best Local Similarity 2.0%; Pred. No. 2.7e-08; Matches 7; Conservative 221; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1344 CATTAGTTTGGAAGCAAATGCTATGGAGGGTTGGAGAAGATAAAGAG 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSASESO for Windows Version 2.0
CURTENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,137
FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Ve., Henry
TITLE OF INVENTION: CAF1-RELATED PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTURELL DELL STATE STAT
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US-09-027-137-2/c
; Sequence 2, Application US/09027137
; Patent No. 6013450
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharm
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
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COUNTRY: US
ZIP: 94304
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                                                                              Length 2852;
                                                                          Score 45; DB 3; Length 285
Pred. No. 0.014;
0; Mismatches 65; Indels
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APPLICANT: Miller, LOUIS H.; ADAMS, JOHN H.; KASLOW,
DAVIC C.; FANG, XIANGDOUG
FILE TITLE OF THE TRANSPORD FOR SEQUENCES: 27

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44.8; DB 4;
Pred. No. 0.011;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
TITLE OF INVENTION: Dromoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER PPLICATION NUMBER: GB 9606062.9
EARLIER PPLICATION NUMBER: GB 9606062.9
EARLIER FILING DATE: 1996-03-22
NUMBER: OF SEQ ID NOS: 89
SCOTWARE: Patentin Ver. 2.1
SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                      1573 ATGTTTTCAGTTATTAAAAAAAAAAAA 1601
                                                                                                                                                                                                                                                                                                                                                            2479 TTTATTTTACAAATTAAAACATAAATA 2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/554,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 64, Application US/08821994A
Patent No. 6228643
GENERAL INFORMATION:
                                                                              2.8%;
56.4%;
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Best Local Similarity 59.4<sup>†</sup>
Matches 76; Conservative
                                                                            Query Match 2.8
Best Local Similarity 56.4
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Brassica napus
US-08-821-994-64
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2229466
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US-08-821-994-64/C
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US-09-027-137-2
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us-08-894-356c-3.rni

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APPLICANT: Allen, Stephen M. APPLICANT: Sakai, Hajime
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Best Local Similarity 58.55
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: CDNA
US-08-545-1968-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1442 TAGAAAAAA 1433
                     1595 AAAAAAAAA 1604
                                                            1442 TAGAAAAAA 1433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-370-253-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                            q
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                                                                                                                                                                                                                             1503 TTTCCTTTTATTGTTTTCTATGTTTTTTCTTTCTTGTACGTTATGAAGAGAAACCGAGTA 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1535 CITGTACGTTATGAAGAAACCGAGTATAAAGGAATAATGTTTTCAGTTATTAAAAAAA 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1475 TGTATGTTTATTTTTTGGAGGGGTTCTTTCCTTTTATTGTTTTCTATGTTTTTTCTTT 1534
                                                                                                                                                                    Gaps
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APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                       Query Match 2.7%; Score 43.8; DB 6; Length 3157; Best Local Similarity 64.1%; Pred. No. 0.031; Matches 66; Conservative 0; Mismatches 37; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 2.7%; Score 43.6; DB 3; Length 1582; Best Local Similarity 58.5%; Pred. No. 0.025; Matches 76; Conservative 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
CLASSIFCATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: FARATION NUMBER: 2121-110P
REGISTRATION NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 205-8000
TELEPAX: (703) 205-8000
TELEPAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
TYPE: nucleic acid
STRANDEDNES: double
                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-545-196B-10/c
; Sequence 10, Application US/08545196B
; Patent No. 6080571
; GENERAL INFORMATION:
FILING DATE: 20-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: CDNA US-08-545-196B-10
               ; SEQ ID NO:3:
; LENGTH: 3157
5198347-3
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1535 CTTGTACGTTATGAAGAGAANCCGAGTATAAAGGAATAATGTTTTCAGTTATTAAAAAA 1594
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                                                                            GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MINNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43.6; DB 3; Length 1582;
Pred. No. 0.025;
0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                    LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US,08/545,196B FILING DATE: 19-OCT-1995
                                                                                                                                                                                                                           ISEE: BIRCH, STEWART, KOLASCH AND BIRCH, PO BOX 747 FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 2121-110P
REEFERDCOMCUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
RESULT 6
8.08-08-5196B-12/c
5.8equence 12, Application US/08545196B
7.Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/09370253
; Patent No. 6165792
; GENERAL INFORMATION:
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REGISTRATION NUMBER: 31,196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTATTATGAGCTGCTATGACTCACATGCATGTATGTTTATTTTTTTGGAGGGGTTCT 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van Emmelo, John
APPLICANT: Van Emmelo, John
APPLICANT: Van Montagu, Maria Helena
APPLICANT: Van Montagu, Maria Helena
APPLICANT: Van Montagu, Maria TITLE OF INVENTION: FLANTS WITH MODIFIED FLOWERS, SEEDS OR
TITLE OF INVENTION: EMBRYOS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1104
CITY: Alexandria
STATE: Virginia
STATE: Virginia
STATE: Virginia
STATE: Virginia
STATE: Virginia
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 1882;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 43.6; DB 4; Length 1
Pred. No. 0.027;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARES PATENTIA Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,467B
FILING DATE: 22-DEC-1994
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US/08/14/92
FILING DATE: 04-APR-1991
PRIOR APPLICATION NUMBER: WO PCT/EP90/01275
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 89 402 224.3
FILING DATE: 04-AUG-1999
ATTORNEY/AGENT INFORMATION:
                                              FILE REFERENCE: BB-1200
CURRENT APPLICATION NUMBER: US/09/370,253
CURRENT FILING DATE: 1999-08-09
FEARLIER APPLICATION NUMBER: 60/097,222
EARLIER FILING DATE: August 20, 1998
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
LENGTH: 1882
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Amino Acid Transporters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 57.2%;
Matches 79; Conservative
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                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Hordeum vulgare
US-09-370-253-1
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US-08-361-467B-4/C
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1473 CATGTATGTTTATTTTTTTGGAGGGGTTCTTTCCTTTTATTGTTTTCTATGTTTTTTCT 1532
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                                                                                                                                                                                                                                                                                                                                                                                Length 1046;
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VENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
VENTION: EMBRYOS
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILING DATE: 7-JUNE-1995
CLASSIFICATION.
                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.7%; Score 43.4; DB 1; Best Local Similarity 57.9%; Pred. No. 0.023; Matches 77; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BURNS, DOANE, SWECKER 6 MATHIS STREET: P.O. BOX 1404
CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
    010830-027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,467
APLICATION NUMBER: US 08/361,467
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Emmelo, John
De Oliveria, Dulce E.
De Souza, Maria-Helena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4, Application US/08484332C; Patent No. 5767374
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: De Greef, Willy
APPLICANT: Van Emmelo, John
APPLICANT: De Olivaria, Dulor
APPLICANT: De Souza, Maria-H
APPLICANT: Van Montagu, Marc
                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
                                                                                                                                         LENGTH: 1046 base pairs
                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PLA
TITLE OF INVENTION: EMI
NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1593 AAAAAAAAAAA 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          922 GAGAGAACAAAA 910
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CLONE: 3C9
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1470 ATGCATGTATGTTTTTTTTTTTGGAGGGGTTCTTTCCTTTTATTGTTTTCTATGTTTTT 1529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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APPLICANT: PERL, ANDRAS
TITLE OF INVENTION: HUMAN TRANSALDOLASE: AN AUTOANTIGEN WITH
TITLE OF INVENTION: A FUNCTION IN METABOLISM
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7%; Score 43.2; DB 2; Length 1:
57.4%; Pred. No. 0.029;
Live 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY: USA

ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,119A
FILING DATE: 19-OCT-1934
CLASSIFICATION: 4355
COUNTY APPLICATION: A355
COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: LIVNAT, SHAUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 280932000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEFX: 90-4039
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2000 Pennsylvania Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08326119A Patent No. 6018021
                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS.
LENGTH: 1332 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1332 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1590 AAAAAAAAAAAA 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1210 GCAAATTTTACATAA 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.4%
                                                                                                                                                                                                                                                                                 CDS
57..1064
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   90-4030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-326-119A-1/C
                                                                                                                                                                                                                                                                         : NAME/KEY:
: LOCATION:
US-09-057-762-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
COCATION:
US-08-326-119A-1
   TELEX:
                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1533 TTCTTGTACGTTATGAAGAGAAACCGAGTATAAAGGAATAATGTTTTCAGTTATTAAAAA 1592
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Patent No. 5879009
GENERAL INFORMATION:
APPLICANT: PERL, ANDRAS
TITLE OF INVENTION: HUMAN TRANSALDOLASE: AN AUTOANTIGEN WITH
TITLE OF INVENTION: A FUNCTION IN METABOLISM
NUMBER OF SECU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.7%; Score 43.4; DB 1; Length 1046; Best Local Similarity 57.9%; Pred. No. 0.023; Matches 77; Conservative 0; Mismatches 56; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/057,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Avenue N.W. STATE: D.C. STATE: D.C. COUNTRY: USA ZIP: 20006-1812 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                         FILING DATE: 04-AUG-1989
ATTORNEY AGENT INFORMATION:
NAME: SCHULMAN, RODERT M.
REGISTRATION NUMBER: 31,196
REFERENCE/DOCKET NUMBER: 010830-093
TELECOMMUNICATION INFORMATION:
TELEFANNE: (703) 836-6620
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 280932000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 872-0168
EP 89 402 224.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,119
FILING DATE: 19-CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
INMEDIATE SOURCE:
CLONE: 3C9
US-08-484-332C-4
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   APPLICATION NUMBER:
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2227 AAGAGGTACCAGAAGAAGTGGAAGAGGTACCAGAAGAAGTGGAAGAGGTACCAGAAGAAG 2286
                                                                                                                          TGGAATACGACGATGACATGGATGGTGTAGAGGTGACAGTGGCTGTTGCAGAAGAGATAG 406
                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08719822B
Patent No. 5874527
GENERAL INFORMATION:
APPLICANT: Barnwell, John
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 10022-7513

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 09/30/96

CLASSIFICATION: 435

ATORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda
REGISTRATION NUMBER: 29,714
REPERBENE/ADCKET NUMBER: 5986/17686US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/719,822B
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Darby and Darby STREET: 805 Third Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.6%;
illarity 51.3%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
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                                                                                                                                                                                                                14 | 14
2347 CAGCGGTAG 2355
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CLONE: PVMB3.3.1
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Matches 97; Conserv
                                                                                                                                                                                              407 AAGTTGCAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                   RESULT 13
US-08-719-822B-1
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                                                                                                                          1530 TCTTTCTTGTACGTTATGAAGAAACCGAGTATAAAGGAATAATGTTTTCAGTTATTAA 1589
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                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Barnwell, John
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby and Darby
STREET: 805 Tarby and Darby
STREET: New York
STATE: New York
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                           Query Match 2.7%; Score 43.2; DB 3; Length 1332; Best Local Similarity 57.4%; Pred. No. 0.029; Matches 78; Conservative 0; Mismatches 58; Indels 0.
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Pred. No. 0.11;
0; Mismatches 92; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08072610
Patent No. 5532133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212,
TELEFAX: 26867
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3337 base pairs
"VPE: NUCLEIC ACID
"VPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                          1590 AAAAAAAAAAAAA 1605
                                                                                                                                                                                                                                                                               1210 GCAAATTTTACATA 1195
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Best Local Similarity 51.3
Matches 97; Conservative
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CLONE: PVMB3.3.1
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                                                                    227 AAGGTGCTGAAAACTTTGACGAGACGTGGAAAAAATTAAAGATGGACTGGCCTTAGTAT 286
Length 3337;
   DB 2;
Score 41.8; DB
Pred. No. 0.11;
0; Mismatches
                 0.11;
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227 AAGGTGCTGAAAACTTTGACGAGACGTGGAAAAAATTAAAGATGGACTGGCCTTAGTAT 286

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Search completed: November 5, 2001, 18:04:28 Job time: 15068 sec
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Best Local Similarity 64.6%;
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                             2347 CAGCGGTAG 2355
                                                                                                                                        407 AAGTTGCAG 415
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US-08-557-309B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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2287 TGGAAGAAGTGGAAGAAGTAGAAGTAGAGGTACCAGCGGTAGTAGAAGTAGAAGTAC 2346
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                                                       347 TGGAATACGACGATGACATGGATGGTGTAGAGGTGACAGTGGCTGTTGCAGAAGAGATAG 406
                                                                                                                                                                                                                                                                   Sequence 1, Application US/09092458

Petent No. 621861

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby and Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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51.3%; Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTONOMY.

NAME: GOGOTIS, Adda
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 5986/17686US3
TREECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/719,821
FILING DATE: 09/30/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 12-7
TELEX: 236687
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3337 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Plasmodium vivax
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 51.3%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10022-7513
COMPUTER READABLE FORM:
                                                                                                                                                                           2347 CAGCGGTAG 2355
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                                                                                                                                  407 AAGTTGCAG 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                    SULT 14
-09-092-458-1
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PREVENTION OF
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                                                               2287 TGGAAGAGTGGAAGAAGTAGAAGTAGAGGTACCAGCGGTAGTAGAAGTAGAAGTAC 2346
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347 TGGAATACGACGATGACAAGGATGGTGTAGAGGTGACAGTGGCTGTTGCAGAAGAGATAG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 0.052;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FUAM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/557,309B
FILING DATE: 14-NOV-1995
CLEASIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422
REFERENCE/DOCKET NUMBER: 20121.422
REFERENCE/DOCKET NUMBER: 20121.422
REFERENCE/DOCKET NUMBER: 20121.422
REFERENCE/DOCKET NUMBER: 20121.422
REFERENCE/CONTONING NUMBER: 20121.422
REGURANTONING NUMBER: 20121.422
REPRENCE/CONTONING NUMBER: 20121.422
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208-557-309B-22/c
; Sequence 22, Application UE/08557309B
; Patent No. 5916572
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em_esthum15:*
em_esthum16:*
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em_estin1:*
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em_esthum12:*
em_esthum13:*
em_esthum14:*

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(without alignments)
2608.282 Million cell updates/sec
                                                                                                                  November 5, 2001, 18:00:43; Search time 5816.79 Seconds
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                          10228115 segs, 4726426750 residues
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                               IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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9b_est2:*
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9b_est4:*
9b_est5:*
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em_esthum5:*
em_esthum6:*
em_esthum7:*
em_esthum9:*
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Maximum DB seq length: 2000000000
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Perfect score:
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em_estpl6:*
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em_estpl3

em_estom2: em_estov1: em_estov2: em_estp11: em_estp12:* em_estro19:*
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em_gss_hum5

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em_gss_pln1:*

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gb_gss3:* gb_gss4:*

gb_gss5:

gss6_dp gb_gss7 gb_gss10:*
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: 6ssb_dp

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gb_gss26 gb_gss28

gb_gss27

gb_gss25

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gb_gss18: gb_gss19:

gb_gss17

gb_gss15: gb_gss16:

gb_gss14

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9b_est52:*

9b_est53:*

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gb_est108:'
gb_est109:'
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. gb_gss36:* gb_gss37:*

em_gss_rod6

gb_gss32:* gb_gss33:*

gb_gss30: gb_gss31:

gb_gss29

TITLE Generation of ESTs from potato leaves and petioles JOURNAL Unpublished (2000) COMMENT Contact: Cathy Rouning The Institute for Genomic Research For clone request: plasse contact Research Genetics, Libraries	FEATURES Location/Qualifiers source 1.632	/organism="Solanum tuberosum" /cultivar="Kennebec" /db_xref"=taxon:4113" //lone="cqRp7R"	/clone_lb="potato leaves and petioles" /clone_lb="potato leaves and petioles" /clone_lb="leaflets and petioles"	/uev.Stage="0 weeks old pignits" /lab_host=="SOR" /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:	Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old	greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."	BASE COUNT 183 a 181 c 95 g 173 t ORIGIN	26.78;	Similarity 81.2%; Pred. No. 3.6e-95; 7; Conservative 0; Mismatches 115;	843 CTCAGGAGACGCCATTCTCCACAATCCAATCACTCCGCACACGTGTGGCTAGCCGT	631 CTCAAATACGCCGTCGTTCTCTACTTTCCAGTCCCTCTCCGCACACGTGTGGCTAGCTGT	QY 903 CACACGTGCGCGCCAAGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTG 962 	Oy 963 CAGGAAAAGGTTGATCCTCCAAATGCCAGAAAGTTACTTCGGCAACCTAATTCAGGCAAT 1022	OY 1023 TITCACAGTGACCGGGCAG3TITGITACTACCAAGCCCGATCGAGTCGAGTGGT 1082	1083 GATACAACAAGCGTCGTGAAGCATGACGCTAAGGCCATTGATGAAGAAGAAGAAGAGTG	Db 391 GATTCAGCAAGCAATTGTGAATGCAGGAGGCGATTGATGAAGGAACAAGGAGTG 332	Qy 1143 GGAGAGCAACCGAAGATCTTTCAGTACAAGATGCTGGAGTGAACTGTTGCTGTTGG 1202 	QY 1203 AAGTTCGCCAAGGTTCAAGGTTACCACGCGGATTTTGGATGGGAAAGCCACAGAGTGT 1262	Db 271 AAGTTCGCCGAGGTTTAAGGGGTATGATGTGGATTTTGGATGGGAAAACCGGAGATAGT 212	QY 1263 GAGGAGTGGTTCGAACAATAGGTTGATGGTGTATTTGTACCAAGGCAAAAATGG 1322	1323 AGGAAGAATGATTGATTAGATTAGTTTGGAAGCAAATGCTATGGAGGTTGGAGA 1	Db 151 AGGAAGAGGAATTGATGTGGAGATTAGCTTGGAAATGCTATGGAGAGTTGGAGA 92	OY 1383 AGATAAAGACTTCCTCATGGAAACTCCTTAATTTGCTTAGCTTGGACTCAACTGGCTACA 1442 	Qy 1443 CTTTATTTATGA 1454	
Description	BE919635 EST423404 AW649974 EST328428	BG126859 EST472505 BF051093 EST436268 BE919634 EST423403 AW928744 EST437532	A172074 E37375554 BG129408 EST475054 AW618433 EST320419 BEG00056 BEG000131	AW039511 EST281792 AW649611 EST328065	BF275133 GA Eb002	AW041172 EST284036 AW617090 EST323501 BE458676 EST413968	BG096122 EST460641 BE924264 EST428033	BC33229 EST400301 BG446054 GA_Ea003 Aw731285 GA_Ea003	BF054047 EST439277 AW399481 EST309981	AW608323 GA_EGU01 AW617259 EST323670 BG441719 GA_EG001	AW/28139 GA_E3UUL AI899779 SD92f04.y	AW735992 EST336760 BG441701 GAEa001 AI730615 BNLGH141	AND 1735 ESTA 1920 BF053972 ESTA 19202 AI727325 BNLGH1775 AW616992 EST3 23403	A1730339 BNLGH1668 AW690825 NF035011S AW399665 EST310165 AT901068 SC19011 V	A1730449 BNLGH1720 BF268244 GA_Eb000	AI730451 BNLGH1721 BF278351 GAEb003 AW934606 EST353498	AI730368 BNLGH1675			EST 02-OCT-2000 Solanum tuberosum cDNA clone			; Embryophyta; Tracheophyta; ledons; core eudicots; lanaceae; Solanum.	 Holt, I.E., Liang, F., Cho, J., Bougri, O., Buell, C.R., Ronning and Baker, B. 	
SUMMARIES Length DB ID	141	143	118	110	143	118 118 167	142	153	143 115	153	103	153	508 118 AW616992	24 119 115	146	24 146 122	24 AI730368	ALIGNMENTS		632 bp mRNA potato leaves and petioles sequence, mRNA sequence.	GI:10445711	tuberosum	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Hagnoliophyta; eudicotyledons; core en Asteridae; euasterids I; Solanales; Solanaceae; Solan	<pre>1 (Dasses 1 to 632) van der Hoeven,R.S., Bezzerides,J., Ho Utterback,T., Hansen,C.L., Doan,B., Bo .C.M., Fry,W.E., Tanksley,S.D. and Bak</pre>	
Result Ouery	428 26	406.4 25 404.2 25 403 25 401.8 25	386.8 24 371.4 23	355.4 22 355.2 22	353.8 22	343.8 21 332.2 20 331.2 20	326 20	315.2 19 315.2 19	314.4 19 306.6 19	305.6 19	301.2 18	300.4 300.2 298.2 18	33 296.4 18.5 34 294.4 18.3 35 294.2 18.3	288.6 18 287.2 17 283.4 17 283.4 17	281.6 17 279.8 17	273.8 17 273.8 17 271.6 16	268.4 16		RESULT 1	BE919635 EST423404 CSTB2C8 3'	ACCESSION BE919635.1	Σ.		KEFEKENCE 1 (Dases AUTHORS van der Ho Utterback,'	

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BG126859 649 bp mRNA EST 31-JAN-2001
EST472505 tomato shoot/meristem Lycopersicon esculentum cDNA clone
CTOF13L13 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum
Bukaryota, Vilidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xhol; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon.

1 (bases 1 to 649)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T., Hansen, C., Ronning, C. and Tanksley, S. Generation of ESTs from tomato shoot/meristem tissue Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon esculentum"
/cultivar="TA4466"
/db_xref="taxon:4081"
/clone="cope1313."
/clone_lib="tomato shoot/meristem"
/tssue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                                                                                                          630 CACCTCAATTTCTGTCCCACCATTCCTTGAACGAACCAAGGCTCGTAACACTCGAGTCAA 689
                         510 TGTGCAGCTCACCAAGCTCAAGGACGGCCTCACCATGGGATTAGCATTTAACCATGCTGT
                                                                                                                                                                                                   570 GCTGGATGGTACTTCGACGTGGCACTTTATGACCTCGTGGTCCGAGCTTTGCTGTGGGTC
                                                                                                                                                                                                                                                                                         393 TGCAGAAGAGATAGAAGTTGCAGATCTTACTG----ATGAAGAAGGCACCACCACAAATTGCA
                                                                                    450 GGACTTGATTCCTTGTAATAAAATCTTGAATTTGGAAGGGCTTCATCGCCCTCTTCTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           690 GCTCAACCTCTCAACCATCAGATGCACCCGAACATGCTA 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG126859.1 GI:12627047
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Matches 514; Conservative
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DEFINITION
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG126859
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Jaclas, J. Vrebalov, J., White, R., van der Hoeven, R.S, Holt, I.E.,
Liang, F., Hansen, T. S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Giovannoni, J.J., Martin, G.B. and Tanksley
                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="tomato germinating seedlings, TAMU"
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/note="Vector: pBlueScript SK('); Site_l: EcoRl; Site_2:
Xhol; 7 days post imbibition on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
to two centimeters in seeds not showing obvious signs of
germination were discarded."

120 c 147 g 178 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 TACAAAAGTGAAAAGTCCTGAAAAAAAAAACAAACGTGAAACCACATAAACCACTAGGAAAAAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 AGAGTGTCAATTGGTAACATTTGATCTTCCTTACCTAGCTTTCTATTACAACCAAAAATT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 TCTCATCTATAA---AGGTGCTGAAAACTTTGACGAGACGGTGGAAAAATTAAAGATGG 272
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                                                                                                          TAMU Lycopersicon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 3.1e-93;
0; Mismatches 118; Indels
                                                                                                      EST328428 tomato germinating seedlings, TAMU Lyco esculentum cDNA clone cLEI11G6 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation of ESTs from germinating tomato seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4081"
/clone="cLEI11G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                          Lycopersicon esculentum
                                                                                                                                                 AW649974
AW649974.1 GI:7411212
                                                                                    657 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 517; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prime sequence.
                                                                                                                                                                                                                                                                                                                                Lycopersicon.
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                                        RESULT
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Gaps

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182 622 242 682 302 742

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196

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/db_xref="taxon:4081"
/db_xref="taxon:4081"
/clone="clEM21F13"
/clone="lb="clonatod"
/clone=lb="clonatod"
/clone=lb="clonatod"
/tissue_type="fruit"
/dev_stage="lmmature green (5-35 days post-anthesis)"
/dev_sta
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EST423403 potato leaves and peticles Solanum tuberosum cDNA clone
CSTB2C8 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 ATGCGTGACAGGGTGTTCAAGTTTTCCGAATCAGCAATTGATCAAATCAAGTCAAAAGTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GCGCGGAACATGCCAAGTCGGAACGAGGGGACGTTAGCGCCAGGGTCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGATCGAGTTCGCTGGTGGATGATACAACAACGATCGTGAAGCATGACGTAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 CCGATTGAGTTTGCGGCAGGGATGATTCATCAAGCCATAGCGAAGCACGATGCGAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTGATGAAAGAAAGAAGTGGGAGAGCAACCGAAGATCTTTCAGTACAAAGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGATGGGGAAAGCCAGAGAGTGTGAGGAGTGGTTCGAACAATAGGTTTGATGGAATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 775 CTTCGCGAAAGAGTATICAAGTTCTCCGAGTTAGCAATTGACAAATCAAGTCAACAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGCCAACTCAGGAGA .....----GACGCCATTCTCCACTTCCAATCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCGCACACGTGTGGCTAGCCGTCACACGTGCGCGCCAACTCAAGCCCGAGGACTACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 ATTGAAGAAAGGAACAAGGAATGGGAGAGTAGTCCGAAGATATTTGCGTACAAAGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACCCGAACATGCTANGTCAGCAACCAACGGTGATGTCCCGGCCAACGTAGACCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1300 TATTTGTACCAAGGCAAAATGGAGGAAGAAGCATTGATGT 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 404.2; DB 143;
Pred. No. 2.7e-89;
0; Mismatches 123; I
  esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE919634.1 GI:10445710
                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 25.2%;
al Similarity 78.5%;
503; Conservative
                                                                                                                                                                                                                                                                                                                                      179
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Best Local S
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nlerman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids i; Solanales; Solanaceae; Solanum;
                                                                                                  121
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                                                                                                                                                                                                     181
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                                                                                                                                                CGAGTCAAGCTCAACCTCTCTCAACCATCAGATGCACCCGAACATGCTAAGTCAGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GACGCCATTCTCCACATTCCACTTCTCCGCACACGTGTGGCTAGCCGTCACA
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                                                                                                                                                                                                                                                      CATGCTGTGGTGGTACTTCGACGTGGCACTTTATGACCTCGTGGTCCGAGCTTTGC
                                                                                                                                                                                                                                                                                                                                                           AACGGTGATGTCCCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAAGTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTTAGCAATTGACAAAATCAAGTCAACAGTCAATGCCAACTCAGGAGA-----
GTGGATGAGCCTCAAGAAATTCAAGTTGCTAATCTTACTGATCATCATGAAGGGATCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAGGGTTGATCCTCCAATGCCAGAAAGTTACTTCGGCAACTAATT 1014
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Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Email: dfrisch@CLEMSON.EDU.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon
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481

601

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

DEFINITION ACCESSION VERSION

BF051093

ORGANISM

KEYWORDS SOURCE

421

301

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299 ATCAACTAGCTGGGAAACTTGGAAAAGATGAAGAGGGGTTTTCAGGGTGGAATACGACG 358
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          Exaryotato.

ESM Solanum tuberosum
Exaryotato.

Exaryotato.

Solanum tuberosum
Exaryotato.

Solanum tuberosum
Exaryotato.

Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum.

NCE I (basea I to 588)

ORS van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning
C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

C.M., Fry, W.E., Tanksley, S.D.

C.M., Fry, W.E., Tanksley, S.D.

C.M., Fry, W.E., Tanksley, S.D.

C.M., Fry, W.E.

C.M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Mol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in limit attorem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 TTCCTTACCTAGCTTTCTATTACAACCAAAATTTCTCATCTATAA---AGGTGCTGAAA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACCTTACTTAGCTTTTTATTATAACCAAAAGTTGATGGTTTACAAATTAGGGACTGAAA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CAAATGTGAAGCCTCAAAAACCACTAGGAAAAAAAAAAGAATGTCAATTGGTAACATTTGATT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTTTGACGAGACGGTGGAAAAATTAAAGATGGACTGGCCTTAGTATTGGTGGATTTCT
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.1%; Score 403; DB 141;
82.8%; Pred. No. 5.3e-89;
live 0; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB2C8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 liquid nitrogen
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Matches 48
                                                   ORGANISM
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JOURNAL
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KEYWORDS
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To (bases 1 to 614)

van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eŭkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /close_lib="tcmatc flower buds 8 mm to pre-anthesis, /close_lib="tcmatc flower buds 8 mm to pre-anthesis, /tissue_type="flower" flower flower buds 8 mm-to-preanthesis" /dev_stage="buds 8 mm-to-preanthesis" /fore="wetcor: pBlueScript SK(-); Site_l: EcoRl; Site_2: Xhol; supplier: Tanksley; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                   AMY28/44 614 bp mRNA EST 30-MAY-2000 EST337532 tomato flower buds 8 mm to pre-anthesis, Cornell University Lycopersicon esculentum CDNA clone CTOC2P16 5', mRNA
                                 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 TTCCTTACCTAGCTTTCTATTACAACCAAAAATTTCTCATCTATAA---AGGTGCTGAAA 238
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482 TCATGACTTCCTGGGCCCAGCTTTGTAGTGGGGCCACCTCCATTTCGGTCCCACCTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 112; Indels
                                                                                                                               TTGAACGAACCAAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                       AW928744 614 bp mRNA
EST337532 tomato flower buds 8 mm to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers.
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476 362 536 422

302

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DEFINITION

BG129408

RESULT

ACCESSION VERSION KEYWORDS ORGANISM

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Lycopersicon.

1 (bases 1 to 582)

1 (bases 1 to 582)

Liang, J., Vrebalov, J., White, R., Matern, A.L., Lakey, J., Holt, I.E., Liang, F., Hansen, T.S., Upton, J., Ronning, C.M., Craven, M.B., Fujii
C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Glovannoni, J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon pennellii
Rukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW618433 582 bp mRNA EST 24-MAR-2000 EST320419 L. pennellii trichome, Cornell University Lycopersicon pennellii cDNA clone cLPT13E7 5', mRNA sequence.
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                                                                                                                                                               181 CTTCCTTACCTAGCTTTCTATTACAACCAAAATTTCTCATCTATAA---AGGTGCTGAA 237
                                                                                                                                                                                                                                                                                                           TATCAACTAGCTGGGAAACTTGGAAAAGATGAAGAAGGGGTTTTCAGGGTGGAATACGAC 357
                                                                                                                                                                                                                                                                                                                                              181 TATCAACTTGCTGGAAAATTGGGAAAAGATGATGAAGGAGTATTTAAGGTGGAATATGAT 240
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                                                                                       122 CAAACGTGAAACCACATAMACCACTAGGAAAAAAG-AGTGTCAATTGGTAACATTTGAT 180
                                                      Gaps
                                                                                                                         9
                                                                                                          CTTACTG - - - ATGAAGAAGGCACCACCAAATTGCAGGACTTGATTCCTTGTAATAAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTGAACGAACCAAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCTCAACCATCAGAT
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                                                                                                                                                                                                                                                                                                                                                                                  GATGACATGGATGGTGTAGAGGTGACAGTGGCTGTTGCAGAAGAGATAGAAGTTGCAGAT
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                                                      Indels
                  DB 174;
                               , 5e-85;
les 122;
                24.1%; Score 386.8;
79.8%; Pred. No. 5.5e
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon pennellii.
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AW618433.1 GI:7324679
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Unpublished (1999)
Contact: David Frisch
                                   Best Local Similarity 79.8
Matches 519; Conservative
                    Query Match
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SOURCE
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1 (bases 1 to 651)

S van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T., Hansen, C., Ronning, C. and Tanksley, S.

Generation of ESTs from tomato shoot/meristem tissue
Unpublished (2001)

Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG129408 651 bp mRNA EST 31-JAN-2001
SEXT475054 tomato shoot/meristem Lycopersicon esculentum cDNA clone
CTOF24G12 5' sequence, mRNA sequence.
BG129408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xhol; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                /clone_llb="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                241
                                                                                      301
                                                                                                                         475
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
TTACTG---ATGAAGAAGGCACCAACAATTGCAGGACTTGATTCCTTGTAATAAAATCT
                                                                                                                                              TGAATTTGGAAGGGCTTCATCGCCCTCTTCTAGCTGTGCAGCTCACCAAGCTCAAGGACG
                                                                                                                                                                                                                     GCCTCACCATGGGATTAGCATTTAACCATGCTGTGCTGGATGGTACTTCGACGTGGCACT
                                                                                                                                                                                                                                                                                          TTATGACCTCGTGGTCCGAGCTTTGCTGTGGGTCCACCTCAATTTCTGTCCCACCATTCC
                                                                                                                                                                                                                                                                                                                                                                 ATGACATGGATGGTGTAGAGGTGACAGTGGCTGTTGCAGAAGATAGAAGTTGCAGATC
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/cultivar="74496"
/db_xref="taxn:4081"
/clone="cTOF24G12"
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source

FEATURES

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

BASE COUNT ORIGIN

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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Mol; Hissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and greenhouse grown plants. The tissue was immediately frozen in limid attoren.
                                                                                                             Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 569)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougril, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of Ests from potato leaves and petioles
 EST424131 potato leaves and petioles Solanum tuberosum cDNA clone
                                                                                                                                                                                                                                                                                                         Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 TACAAAAGTGAAAGTCCTGAAAAAAAACAAACGTGAAACCACATAAACCACTAGGAAAAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 AGAGTGTCAATTGGTAACATTTGATCTTCCTTACCTAGCTTTCTATTACAACCAAAAATT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 AGAATGTCAATTGGTAACATTTGATTTACCTTACTTAGGTTTTTATTATAACCAAAAGTT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 TCTCATCTATAA--; AGGTGCTGAAAACTTTGACGAGACGGTGGAAAAAAATTAAAGATGG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 GATGGTTTACAAATTAGGGACTGAAAACTTTGAGGAAACAGTGGAAAAATTGAAAGATGG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 AGGGGTTTTCAGGGTGGAATACGACGATGATGGATGGTGTAGAGGTGACAGTGGCTGT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 TGCAGAAGAGATAGAAGTTGCAGATCTTACTG----ATGAAGAAGGCACCACCAAATTGCA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 GGACTTGATTCCTTGTAATAAAATCTTGAATTTGGAAGGGCTTCATCGCCCTCTTCTAGC 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 TTTGGCTTTAGTGTTGGAAGATTTTTATCAACTTGCTGGGAAATTAGGAAAAGATGAAGA 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB5F22"
/tlone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 363.6; DB 142;
Pred. No. 2.9e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89;
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/organism="Solanum tuberosum"
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   cSTB5F22 5' sequence, mRNA sequence. BE920362
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Solanum 1
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                                                                                                                                                                                                                                                                                                         /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                         /clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.1%; Score 371.4; DB 118; Length 582; 79.9%; Pred. No. 3.4e-81; 1.1ve 0; Mismatches 111; Indels 6;
                                                                                                                                                                       /organism="Lycopersicon pennelli1"
/db_xref="taxon:28526"
/clone="cLPT13E7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          690 GCTCAACCTCTCTAACCATCAGATGCACCCGAACATGCTA 730
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               Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Clemson University Genomics Institute
                                                                                                                                 Cocation/Qualifiers
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                                                                                           Email: dfrisch@CLEMSON.EDU
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1 (bases 1 to 541)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S, Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronnning,C.M.,
Nierman,W., Fraser,C.M., Giovannoni,J.J., Martin,G.B. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum
Sukaryota: Vilidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/clone="tomato germinating seedlings, TAMU"
/clone=lib="tomato germinating seedlings, TAMU"
/clssue_trype="whole seedlings"
/dev_stage="7 days post imbibition"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; 7 days post imbibition on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
to two centimeters in seeds not showing obvious signs of
germination were discarded."
a 156 c 131 g 120 t
449
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                                                                                                     510 TGTGCAGCTCACCAAGCTCAAGGACGGGCTCACCATGGGATTAGCATTTAACCATGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                     570 GCTGGATGGTACTTCGACGTGGCACTTTATGACCTCGTGGTCCGAGCTTTGCTGTGGGTC
                                                                                                                                                                                                                                                   450 GGACTTGATTCCTTGTAATAAAATCTTGAATTTGGAAGGGCTTCATCGCCCTCTTCTAGC
                                                                                                                                                                                                                                                                          333 AGGGGTTTTCAGGGTGGAATACGACGATGACATGGATGGTGTGTAGAGGTGACAGTGGCTGT
                                                                                                                                                                    393 TGCAGAAGAGATAGAAGTTGCAGATCTTACTGATGAA---GAAGGCACCACAAATTGCA
                                                                                                                                                                                                                                                                                                                                                           AW649611 544 bp mRNA EST304-APR-2
EST328065 tomato germinating seedlings, TAMU Lycopersicon
esculentum cDNA clone cLEI8J16 5', mRNA sequence.
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Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: dfrisch@CLE:MSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 Jordan Hall, Clemson,
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="TA496"
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Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prime sequence.
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AW649611.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 561)
D'Ascenzo, H. He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Ronning,C.M., Craven,M.B., Fujil,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Glovannoni
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                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum
Sukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                         AW039511 561 bp mRNA EST 18-OCT-1999
EST281792 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA
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                                                        22.1%; Score 355.4; DB 110; Length 561; 80.5%; Pred. No. 3e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 prime sequence.
Location/Qualifiers
1.561
/organism="Lycopersicon esculentum"
/cultivar="Rio Grande PtoR"
/db_rare="taxon:4081"
/clone="cLET14C2"
/clone="taxon:4081"
/clone=Lib="tomato mixed elicitor, BTI
/tiswe_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XII-Blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation of ESTs from tomato leaf tissue Unpublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                   clone cLET14C2, mRNA sequence
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AW039511.1 GI:5898265
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( (bases 1 to 556)

van der Hoeven, R.S., Bezzerides, J., Holr, I.E., Liang, F., Cho, J., Utterback, T., Hanssen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Genration of ESTS from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF053244 556 bp mRNA EST 16-OCT-2000 EST438474 potato leaves and petioles Solanum tuberosum cDNA clone cSTB34L5 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               952 TTTGCTGATTGCAGGAAAAGGGTTGATCCTCCAATGCCAGAAAGTTACTTCGGCAACCTA 1011
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                                                                Gaps
                                                                                                                   9
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Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                     1 GGGCTTCATAGGCCTCTACTCGCCGTACAGCTCACCAAGCTTAAAGACGGGCTGGCAATG
                                                                                                                                                                                                                                                                                                                                                                   GTATTCAAGTTCTCCGAGTTAGCAATTGACAAATCAAGTCAAGAGTCAATGCCAACTCA
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                                                             Indels
                                     Score 355.2; DB 119;
Pred. No. 3.4e-77;
0; Mismatches 93;
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                                     22.1%;
80.1%;
                                   Query Match 22.1
Best Local Similarity 80.1
Matches 436; Conservative
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."
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GA_Eb0023D13f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Eb0023D13f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 786)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 TACAAAAGTGAAAGTCCTGAAAAAACAAACGTGAAACCACATAAACCACTAGGAAAAAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 AGAGTGTCAATTGGTAACATTTGATCTTCCTTACCTAGCTTTCTATTACAACCAAAAATT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCATCTATAA---AGGTGCTGAAAACTTTGACGAGACGGTGGAAAAAATTAAAGATGG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACTTGATTCCTTGTAATAAAATCTTGAATTTGGAAGGGCTTCATCGCCCTCTTCTAGC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTGCAGCTCACCAAGCTCAAGGACGGGCTCACCATGGGATTAGCATTTAACCATGCTGT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGGTTTTTCAGGGTGGAATACGACGATGATGGATGGTGTAGAGGTGACAGTGGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAGAAGAGATAGAAGTTGCAGATCTTACTG---ATGAAGAAGGCACCACCAAATTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
9
                                                                                                                                                                                                                                                                                                                                                                                                     Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                       and petioles"
         /cultivar="Kennebec"
/db_xref="taxon.41]3"
/clone="CSTB34L5"
/clone="LD="potato leaves and petioles
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGGATGGTACTTCGACGTGGCACTTTATGACCTCGTGGTCCGA 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 353.8; DB 1 Pred. No. 7.6e-77;
/organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                               158
                                                                                                                                                                                                                                                                                                          130 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF275133.1 GI:11206203
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82.3%;
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ORIGIN
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ORGANISM
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JOURNAL
COMMENT
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                                                   1137
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KEYWORDS
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Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Lupublished (2000)
Contact: Wing RA
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Fax: 864 656 4293
Email: rwingeclemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 719.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:29729"
/clone="GA_Eb0023D13f"
/clone_llb="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGATTGCAGGAAAAGGGTTGATCCTCCAATGCCAGAAAGTTACTTCGGCAACCTAATTCA 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGATTAGCATTTAACCATGCTGTGCTGGATGGTACTTCGACGTGGCACTTTATGACCTC 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ATGGGCGCAAATCTGTAGGGGGTCCAACTCCGTCTCAGTCTCGCCGTTTCTCGAGGGGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCAACCATCAGATGCACCCGAACA 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCATCCGACTCCTCTAAACCATTCTCAACTTTCCAATCTCTAGCTTATCACGTTTGGCA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
206 c 202 g 173 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 | 1111 | 1111 | 1 | 1 | 1 | 1 | 1111 | 1111 | 1 | 1111 | 1 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CAAAGTCCGAAACACCCGCGTGAAGCTGGATCTCTCGCTCCCACCTAACTCTGTCAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGA------GAGACGCCATTCTCCACATTCCAATCACTCTCCGCACACGTGTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGATTGTCGTAAAAGGGTTGATCCACCCATGCCAGAAAGTTACTTCGGAAACCTGATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.5%; Score 345; DB 146; Length 786; Larity 67.6%; Pred. No. 1.2e-74; Conservative 0; Mismatches 225; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="8400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host-"E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="AKA"
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Best Local 3
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                      AUTHORS
                                                                                                                               JOURNAL
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                                                                         TITLE
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/clone_lib="tomato mixed elicitor, BTI"
/tissue_type="leaf"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/dev_stage="4-6 week old plants"
/lab_host="Xi-1-Blue MRF"
/note="vector: pBlueBScript SK(-); Site_l: EcoRl; Site_2:
Xhol; cLET - Inoculated with a variety of disease response elicitors: plants exposed to 2,6 dichloroisonicotinic acid, BTH, jamonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. (bases 1 to 563)
D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Glovannoni
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Sukaryota; Viridizlantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW041172 563 bp mRNA EST 18-OCT-1999
SET204036 tomato mixed elicitor, BTI Lycopersicon esculentum CDNA clone cLET11N19, mRNA sequence.
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                          1197 TGTTGGAAGTTCGCCAAGGTTTCAAGGTTTACGACGTGGATTTTGGATGGGGAAAGCCAGA
                                                                                                                         634 GGTGGGGAGCTCTCCCAGGTTCAAGGTATACGATGTGGATTTCGGGTGGGGAAAACCGGA
                                                                                                                                                                                                                                                      694 AGGGGTGAGGAGCGGATCCAACAACAGGTTTGATGGGATGGTGTATTTGTATCAAGGGAA
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Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4295
Email: dfrisch@CLEMSON.EDU
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Pred. No. 2.2e-74;
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/db_xref="taxon:4081"
/clone="clET11N19"
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van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronling, C.M., Nierman, W., Glovannoni, J.J. and Tanksley, S.D. Generation of ESTs from wild tomato (Lycopersicon hirsutum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eŭkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon hirsutum"
/db_xref="taxon:62890"
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/clone_lib="L. hirsutum trichome, Cornell University"
/tissue_Lype="trichome"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
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                          GATGGTTACAAGTTAGGGGCTGAAAGCTTTGAGGAAACAGTAGAAAAATTGAAAGATGG
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                                                                                                                                               ACTGGCCTTAGTATTGGTGGATTTCTATCAACTAGCTGGGAAACTTGGAAAAGATGAAGA
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Clemson University Genomics Institute
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Location/Qualifiers
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100 Jordan Hall, Clemson, SC
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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5, 2001, 18:00:51

completed: November le: 14891 sec

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nitrogen, shearing off trichomes. This procedure yielded mixture of cells which is highly enriched for trichome likely with minor contaminations of other types of leaf
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Pred. No. 1.6e-71;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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AB026494 E12757 AB010708 E12753 AB016892

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                                                                                                                                                DB 10; Length 1479;
             /organism='Perilla ocimoides'
                                                                                                        others
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                                          1. .1343
/product='acyltransferase'
                                                                                                                                              100.0%; Score 1478.6;
99.9%; Pred. No. 0;
:ive 1; Mismatches
                                /clone='psAT208'
                                                             Location/Qualifiers
1. 1479
/organism="unidentified"
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a 316 c 331 g 411
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                                                                                                                                                        Best Local Similarity 99.9%;
Matches 1478; Conservative
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AC087734 Arabidops
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AC061391 Plasmodiu
AC011391 Plasmodiu
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AC011689 Homo sapi
AC07135 Plasmodiu
AC011689 Homo sapi
AC071381 Homan Cos
AC000110 Human Cos
AC000129 Plasmodiu
AC11257 T7 end of
AC011689 Homo sapi
AC07189 Homo sapi
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CIZNI5/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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PF 30-JAN-1996 JP 1996046534
PR 30-JAN-1996 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashlari, T. Tanaka, Y., Fujiwara, H., Nakao, M., Fukul, Y., Yonekura, K., Mizutani, M. and Kusumi, T. Gene Coding Protein Having ACYL GROUP TRANSFER ACTIVITY Patent: JP 1997070290-A 4 18-MAR-1997;
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AP000606
I 66494
AB006696
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ATF1612
AC069373
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AE001391
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AC087789
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PC (C12N9/10,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key
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Perilla ocimoides mRNA for
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1 (bases 1 to 1479)
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E12756.1 GI:3251588
JP 1997070290-A/4.
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Location/Qualifiers 1. 1476 Organism="Perilla frutescens"	1 1 1 1 1 1 1 1 1 1	09 301 CAGAATCTAGCGACGACTTCGATGATCTCCTCGGAAATCGTCCAGAATCTCCCGTTAGGC 360 11
900 FEATURES SOUIC 900 960 CDS 960 CDS 1020 1020 1140 BASE COUNT 1140 BASE COUNT 1200 Query Ma 1200 GLEGIN 1200 GLEGIN 1260 GL		Qy 301 se, partial Qy 361 rracheophyta; Db 361 licots; Qy 421 licots; Qy 481 ., Fukui,Y., Db 481 oy 541 bb 541 coy 601 bases. Keiko Y Db 601 nr., Plant Qy 661 n, Osaka Oy 661 o, Db 661
0y 841 CATTCACAGCAGATGAGACCAAGACAAGGATGCATTTTCTTGATTCCGGTCGATC 1 111111111111111111111111111111111111	Db	RESULT 2 AB029340 LOCUS AB029340 LOCUS AB029340 DEFILLA frutescens mRNA for anthocyanin acyltransferase, p cds. ACCESSION AB029340. KEYWORDS RETILLA frutescens leaf cDNA to mRNA. AB029340. REFINATION anthocyanin acyltransferase. SOURCE Perilla frutescens leaf cDNA to mRNA. PETILLA frutescens leaf cDNA to mRNA. Perilla frutescens leaf cDNA to mRNA. REFERENCE Perilla frutescens leaf cDNA to mRNA. Spermatophyta: Magnollophyta; eudlocyledons; core eudloct Asteridae; euasterida i; Lamiales; Lamiaceae; Perilla. AUTHORS ANINATIT: Yamaguchi,M. and Kusuni,M.F., Fujiwara,H., Fu ANINALLA and Noblechical characterization of a novel hydroxycinnamoyl-CoA: anthocyanin 3-O-glucoside-6 JOURNAL Unpublished (1999) AUTHORS SAKAKIDATA,K.Y. and Tanaka,Y. TITLE Direct Submission JOURNAL Shakibara, Kultory Research Center, Fundamental Research, Blotech; Shimamoto-cho, Wakayamadai, 1-1-1, Mishima-gun, O 618-8503, Japan (E-mail:Kelko_Sakakibaraésuntory.co.jp, Tel:+81-75-962-8807, Fax:+81-75-962-8802)

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                                                                             topology: Linear;
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                                     TAGTCCATCTCTCTTTTTTTTTTGCAGTTGCAGCTTATATGTGGGGCTGGCATAACGAAAT
                                                                           TAAGGCCACGATTAGATCCGCCGGTTCCTGAAAATTACTTCGGGAACTGCTTATCGTACG
                                                                                                                                                      CGCTGCCGAGAATGCGGCGGCGAGAGCTGGTGGGAGAAAAGGGGGTGTTTCTGGCAGCTG
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TTTTCACCCAATCCAAAATTAAGAAATTGAAGGGTTGGATTCAGTCCAGAGTTCCAAGTT
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T..
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PAtent: JP 1997070290-A 2 18-MAR-1997;
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JP 1997070290-A/2
18-MAR-1997
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                                                                                                                         : FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKA
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10,
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
MASAHIRO,
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                                                                                                                                                                                                                                                                                                                                                       /organism='Gentiana triflora'
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Pred. No. 9.5e-43;
); Mismatches 661; Indels
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/clone='pGAT106'
35. .1474
/product='acyltransferase'
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    1622
    /organism="unidentified"
    /db_xref="taxon:32644"
    345 c 322 g 477

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//Translatio---MAGNSEDIKVLEKCRVAPPDAVAEFTVPLSFFDMRWLISDAEH
HILFYRERPHPCPNSKTISSTKSSLSLIVLKHFPLAGALLUPWDDSSDRWPELKYKGD
SVSLTIAESSMCPPLAGDHQRDSYKENDLIPQLPBEJAGNLUPWDDSSDRWPELKYKGD
SVSLTIAESSMCPPLAGDHQRDSYKENDLIPQLPBEJAGSELPWDLSALDVYTVFSG
SVSLTIAESSMCPPLTAGDHQRDSYKENDLIPQLPBEJAGSELPWDRSVVODPFH
TREKTIVHERKLIKSQCPFTVLMRALSKSDPRAFTLIHPDIMKLKKFTSSKNRMLTGS
SNYNLSFFTVTSALLYTVCLSKSLDTVVREKVEEDKRAANLCAFINGRRFAPPTPQN
PGNCIVPCNVGSTHEQLVGNEGLSVAATAIGDAIHKRLHDYEGILRGDMISPPRSTSA
APRSTLIXVVGSAQRRYHDFDADFGWGKLEKHESVSTNPSATLILISRSRFKGALEL
GISLDRARMADAFATA
312 9 477 t
                                                                                                                                                                                                                      Research;
          Kusumí,T.
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2 (bases 1 to 1622).

Tanaka,Y. and Yonekura-Sakakibara,K.
Direct Submission.
Submitted (21-APR-1999) to the DDBJ/EMBL/GenBank databases. Yoshikazu Tanaka, Suntory Ltd., Institute for Fundamental Fwakayama-dai 1-1-1, Shimamoto, Osaka 618-8503, Japan (E-mail:Yoshikazu_Tanaka@suntory.co.jp, Tel:81-75-962-8807, Fax:81-75-962-8262)
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Yonekura-Sakakibara,K., Tanaka,Y., Fukuchi-Mizutani,M.
Fujiwara,H., Pukui,Y., Toshihiko,A., Yamaguchi,M. and
Molecular cloning and biochemical characteization of
                                                                                                 frutescens and diverse plant acyltransferase homologs
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es 661; Indels
                                                          hydroxycinnmamoyl-CoA:anthocyanin
3-O-glucoside-6-0-hydroxycinnamoyltransferase
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/protein_id="BAA93452.1"
/db_xref="G1:7415597"
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/db_xref="taxon:55190"
35. .1474
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 24-JUN-1998
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PN JP 1997070290-A/5
PD 18-MAR-1996
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHTIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CGTGATCGAAACGTGTAGAGTTGGGCCGCCGCCGGACTCGGTGGCGAATCGGTGCC
                                                                                                                                      1 (bases 1 to 1508)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T..
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 5 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.9%; Score 190.6; DB 10; Length 1508; Best Local Similarity 49.6%; Pred. No. 5.7e-36; Matches 676; Conservative 0; Mismatches 654; Indels 33;
E12757 1508 bp DNA PAT 24-JU
Senecio cruentus mRNA for acyltransferase,,partial cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product='acyltransferase'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism='Senecio cri
/tissue_type='petal'
/clone='pCAT48'
1.1367
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/organism="unidentified"
/db_xref="taxon:32644"
a 293 c 296 g 47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           topology: Linear;
                                                                    JP 1997070290-A/5
                                                                                     unidentified.
unidentified
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TTGCGTCACGGTCCCCACTTTTTTCACTTCAAGTGACGTTTTTTTCCGGGCTCGGGTTTTTT
                                                                                      467 TATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCGTTTATAAC
                                                                                                                 ACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGAA
                                                                                                                                            GCCTTGGTCTTCAATGAGCAAACACATTGAAAATGAAGATGAAGATGAAGAATTTAAAATC
                                                                                                                                                          TTTGCCAGTTTTCGATAGATCCGTCATAAAATATCCGACGAAATTTGACTCCATTTATTG
                                                                                                                                                                                                          GAGAAACGCGCTAAAATTTCCTTTGCAATCTCGTCATCCCTCATTACCGACGGACCGCAT
                                                                                                                                                                                                                                                                  TCGGTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAAAGAAAAAGGTCTTAAC
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AB010708 1679 bp mRNA PLN 20-FEB-1999 Gentiana triflora mRNA for Anthocyanin 5-aromatic acyltransferase, complete cds.

LOCUS

RESULT AB010708

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/translation="megigwvkvlekcqvtppsdttdvelsslpvtffdipwlhlnkwg
sllfydfydfydfydfydlkasislltlkitvplggnllhydrgerpkfoysrdb
gdsttlydfydfydfydlhglydsndlhglfywprvtryddygvyvy
FPNRG1AyALTAHFLADYLKGHQLVDSNDLHGLFYWPRVTRTWGDXVVIPLVAVQVTV
FPNRG1AyALTAHFLADAKSFVMFINAMATTNFGRADLLSANLLPSFDRS1IKDL
YGLEFFWNEWQDVLEMFSRFGSKPPRFNKYRATYVLSLAEIOKLKKKVLNIRGSEPT
IRVTFFYTGCYVWTCWYRSADDVYSESSNDDRDELEYFFFADGRGLTPPQCPNYF
GNCLASCWARATHERLYGDKGLLVAVAAIGERIENTERHEKGVLADAKTWLSESNGIP
SKRFLGITGSPKFDSYGVDFGWGRPAKFDITSVDYAELLIYVIQSRDFFEKGVEIGVSLP
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                                                                                     Tracheophyta;
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Fujiwara,H., Tanaka,Y., Yonekura-Sakakibara,K.,
Fukuchi-Mizutani,M., Nakao,M., Fukul,Y., Yamaguchi,M., Ashikari,T.
                                                                                                                                                                                                                                             Submitted (22-JAN-1998) to the DDBJ/EMBL/GenBank databases. Hiroyuki Fujiwara, Suntory LTD., Inst. of Fundamental Research; 1-1-1, Wakayamadai, Shamamoto-cho, Osaka 618-0024, Japan (E-mail:Hiroyuki Fujiwara@suntory.co.jp, Tel:+81-75-962-8867, Fax:+81-75-962-8262)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 TTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGAC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA cloning, gene expression and subcellular localization of anthocyanin 5-aromatic acyltransferase from Gentiana triflora Pplant J. 16 (4), 421-431 (1998)
                                                                                Eukaryota; Vixidiplantae; Streptophyta; Embryophyta; Tracheor
Spermatophyta: Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Gentianaceae; Gentiana
1 (bases 1 to 1679)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Anthocyanin 5-aromatic acyltransferase"
/protein_id="BAA7428.1"
/db_xref="G1:4185599"
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Anthocyanin 5-aromatic acyltransferase.
Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
Gentiana triflora
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/db_xref="taxon:55190"
                                                                                                                                                                                            Fujiwara, H., Tanaka, Y. and Kusumi, T. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.6%; Score 172.2; 49.5%; Pred. No. 1.8
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350 c 359 g 48
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                                                                         GGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCC 518
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 CCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKA C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10,
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PN JP 1997070290-A/1
PD 18-MAR-1997
PF 30-JAN-1995 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product='acyltransferase precursor'
                                                                                                                                                                                                                         1 (bases 1 to 1703)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 1 18-MAR-1997;
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Location/Qualifiers
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/tissue_type='petal'
/clone='pGAT4'
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/organism="unidentified"
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Lacture (18-AUG-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Departnent of Plant Gene Research; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel: 81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp, Ror the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos@cgi-bin/agd_graph.cgi?c=wxFl2 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.orml.gov/Grail-1.33/, http://ccmaple.car.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.ar.de.
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This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is K15E6 and the 3' clone is K3K3.
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vsgrnwtaehqkilssnlvnasftaqasyqesgvsqipymtarifrseftysfpvtpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridipiantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (sites)
Asamizu,E., Sato,S., Kaneko,T., Nakamura,Y., Kotani,H., Miyajima,N. and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsul Pl
clone:MXF12.
GAAGGCTTTTGCTCTTTGT'CATAGTCTCTTTAATAGAACCATATTTGCTGCAATAAAGTA 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                    27-DEC-2000
5, Pl clone:MXF12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mosome 5. VI
covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structural analysis of Arabidopsis thallana chromosome
Sequence features of the regions of 1,081,958 bp covere
seventeen physically assigned Pl and TAC clones
DNA Res. 5 (6), 379-391 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence~not_experimental
/product~'receptor-like protein kinase"
/protein.id="BAB10834.1"
/db_xref="G1:10177545"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
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                                                                                                                                                                                           1452 CCAAGTCCTTTAGTAACACTACACCCAAACCCTACTTT 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassicales; Brassicaceae; Arabidopsis.
                                                                                                  TTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTAT
                                                                                                                                                                                                                                                                                                                                                Arabidopsis thallana genomic DNA, ABO16892 BA000015
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/note="gene_id:MXF12.2"
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2613. .5234
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/chromosome="5"
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/trānslation="MGNKKLLTGGSSKTHGSGSSYRDPLLQNQEDKPKANGSENGLND
LEHGVVEAANGFGRVFALICQYSSINVSQAKEDAGKLVITALLICSTTALLICSTTHLLVPKF
GGMIIDIUSRDWYFPEQQTEGLIAVRNAVYILLILVGSTCTALRAMLFNGASERVV
ARLRKDLFRHLMHQEIAFYDVTKTGELLSRLSEDTQIIKNAATTNLSEALRNVTTALI
                                                                                                                                                                                                                                                                                                                                                           GVGFWFTSSWKLTLLALVVVPVISVAVKQFGRYLRELSHTTQAAAAVAASIAEBSFGA
VRTVRSFAKESYMVSQYSKKVDETLKLGLKQAVLVGLFFGGLNAAFTLSVITVVSYGA
YLTIYGSMTVGALTSFILYSLTVGSSVSSLSSLYTTAMKAAGASRRVFQILDRVSSMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGDKCPVGNPDGDVELNDVWFAYPSRPSHMTIKGISLRLTPGSKVALVGPSGGGKTT
IANLIERFYDPLKGKILLNGVSLMEISHQYLHKGISTSVGBPTLENGSYEBNIAYGFD
GEASFTDIENAAKMANHEFIBAFPDKYNTVVGERGLRLSGGCRQRIAIARALLTNPS
VLLIDBRATSALDAESEYLVQDAMDSLAAGRYLVIAHRLSTVKTAACVAISDGEVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MYNEEMESSLKVIDVARVTPSNSDSSESLTLPLTFFDLLWYKLH
AVERVIFYKLTDASRPFFDSVIVPNLKTSLSSSLSHYLPLAGKLVWEPLDPKPKIVYT
PNDAVSFTVAESNADFSRLTGKEPFPTTELYPLVPELHVSDDSASAVSFQVTLFPNQG
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CIAGCSRMMLTAKMFMGEEGLLAAATMVSDSIEEWDESFAWKIPDFVATLPPETQL
LILSGSUNFGYVELDFGWGRPDKVMVVSISPGNGISMAESRDGNGSVEIGFSLKKHEM
DLILDLHGELTI"
34363. .35709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYFETFMSEEGFLAAARMVSDSVEALDENVALKIPEILEGFTTLSPGTQVLSVAGSTR
FGVYGLDFGWGRPEKVVVVSIDQGEAISFAESRDGSGGVELGFSLKKHEMDVLVDLLH
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IFYRIINVTRPFFDSVIVPNLKTSLSSCLSHYLPLAGKLIWEPLDHKPTIVYSQNDDV
SFSVAETNADFSSLSGNEPFPSTELYPLYPALQSSDDSASIVSFQVTLFPNQGFCIGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="anthocyanin acyltransferase-like protein"
/protein_id="BaB10829.1"
/db_xref="G1:10177550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/product="anthocyanin acyltransferase-like protein"
/protein_id="BAB10830.1"
/db_xref="G1:10177551"
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complement(join(30804, .30874,30947, .31289))
/note="contains similarity to Ac-like transposase
gene_AG-MXF12.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.5%; Score 110.8; DB 12; Length 66237; llarity 46.5%; Pred. No. 3.1e-16; Conservative 0; Mismatches 662; Indels 48; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(27466. .27879,28046. .29073))
/note="gene_id:MXF12.8"
/codon_start=1
                                                                               transporter-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGTHDELLSLNGIYTNLVKRQLQSSSSVTTL"
join(25348. .26359,26401. .26756)
/note="gene_id:MXF12.7"
                                         /evidence=not_experimental
/product="ABC_transporter-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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                                                                                                        /protein_id="BAB10828.1"
/db_xref="G1:10177549"
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/note="gene_id:MXF12.10"
/codon_start=1
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Best Local Similarity
Matches 616; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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                                                                                                        YDAILNGVEILKANDPDGNLAGPNPDPLVSPDLIPNRATPRIEKNKSHILPITLAVVG
FLYVLAMFVVGVLVIMKKKKSRPSTNSSNGPLPPRTDSTNTRPAKSHILPITLAVVG
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SGSSMGVFSEINEPKAR"
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WTQEEKNILPKNSDNASFSSVVSYKEESGIPQVPYMTARIFRSDFTYSFPVSPGWKFL
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LLDDNFCPRYADFGLAKLCEKRESILSLIDTRYGTIGYIAPEVVSRWYGGISHKSDY
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KMILVSLWCIRPCPSORPPMNKVOEMIEGSLDALELPPKPSRHISTELVLESSSLSDG
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RNWTVESRQILSSNLVNASFTSEASYQKAGVSRIPYMKARIFRSEFTYSFPVTPGSIF
LRLYFYPTQYKSGFDAVNSFFSVKVNGFTLLRNFNADSTVQASIPLSNSLIKEFIIPV
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LATFIVIIMLLIRQMKRKKNKKENSVIMFKLLLKQYIYAELKKITKSFSHTVGKGGFG
TVYRGNLSNGRTVAVKVLKDLKGNGDDFINEVTSMSQTSHVNIVSLLGFCYEGSKRAI
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QNILLDGNLCPKVSDFGLAKLCEKRESVLSLMDTRGTIGYIAPEVFSRMYGRVSHKSD
VYSFGMLVIDMIGARSKEIVETVDSAASSTYPPDMIYKDLEDGEQTWIFGDEITKEEK
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                                 PDDVYATSRSMGNADHPEQNLNFNLTWLFTVDAGFSYLVRLHFCETLSEVNKEGQRVF
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                                                                               SIFIENQTATLEMDVFRMSGSWIPMYLDYTVIAGSGSGRRHDLRLDLHPLVSINPKY
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L. Submitted (26-JAN-1998) Arabidopsis thaliana Genome Center, Submitted (26-JAN-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 101176)

S. Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Chio, J., Choi, E., Chao, C., Khan, S., Kim, C., Alfaffi, H., Bei, B., Chin, C., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukhanssky, N., Nguyen, M., Palm, P., Sakano, H., Schwartz, J., Southwick, A., Thaveria, A., Torium, M., Vaysberg, M., Yu, G., Davis, R., Pederspiel, N., Theologis, A. and Ecker, J.

L. Submitted (28-UNN-2000) Arabidopsis thaliana Genome Center, Department of Buology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, Pa 19104-6018, USA

E. Chases I to 101:76)
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Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome
I, complete sequence.
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I (bases 1 to 101176)

Khan,S., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C., Kim,C., Shinnip,P., Altafi,W., Bel,Q., Chin,C., Chio,U.J., Chol,E., Conn,L., Conway,A., Gonzales,A., Hansen,N., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Federspiel,N.A., Theologis,A. and Ecker,J.R.
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Submitted (13-NOV-1997) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
4 (bases 1 to 101176)
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                                                                                                                                                                                                               AGAGAGGAAAGATATCAATIGCGGAGAGTAGAATGGAAGTGGAGGTGTTGAGATTGGCT
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AC002560.2 GI:92X1167
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REFERENCE AUTHORS

JOURNAL

TITLE JOURNAL

COMMENT FEATURES

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join(11965. .12033,12173. .12303,12448. .12519,12596. .12685,
12756. .12915,12985. .13041)
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LQSSGFCIRRY"
                                                                                                                                                                    MTGEFLEELLSEALGINPUHLKDMGCAKSH INFGQYYPPCPQPDLTGGISKHTDFSF
ITILLQDNIGGLQVIHDQCWVDVSPVPGALVINIGDLLQLISNDKFISAEHRVIANGS
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VGQHYPPCPQPDLTIGINKHTDISFLTVLLQDNVGGLQVFHEQYMIDVTPVPGALVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MNTIVVAQLQRQFQDYIVSLYQQGFLDNQFSELRKLQDEGTPDF
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NVSFKLCENLLVLLLEKQILQAGGTIPQVDIN"
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IQPANQVTISTVDLSYNRFSGGISPLLSSVENLYLNSNRFTGEVPASFVERLLSANIQ
TLYLQHNFLTGIQISPAAEIPVSSSLCLQXNCMVPPLQTPCPLKAGPQKTRPTTQCTE
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KWTRLNPIGDVPSPRACHAALLYGTILILOGGIGFSGPDGDVYMLDMTNKNIKFLV
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VFGGSKLHVIGGILNRARLIDGEAVVADTNQPETSASGANRQNOYQLMRRCHHAAASF
                                                                                                     SMDLI SRRSVVEKIGDAAERWGFFQVVNHGI SVEVMERMKEGIRRFHEQDPEVKKRFY
SRDHTRDVLYYSNIDLHTCNKAANWRDTLACYMAPDPPKLQDLPAVCGEIMMEYSKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                              IGDFLQVKKIMLLLRSCFISCMIWGLILLFYCVQLITNDKFISAEHRVIANGSSEPRT
SVAIVFSTFMRAYSRVYGPIKDLLSAENPAKYRDCTLTEFSTIFSSKTLDAPKLHHFK
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STRFESWDFGSPAGYCKNGWY YSLNLCDMFAGSPGISGRIDPAIGKLSALTEL
STRFESWDFTSOLKDLRFLATSTESFEIPASLGFRTDLSYNGLTGT
ISPSIGSLPELSNLILCHNHLTGSIPPFLSQTLTRIDLKRNSLTGSISPASLQY
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                               /translation="MGHDSFCYLIVLRCALRCGIIALMQICALQKKERRSKMESSDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16495. .17682
//note="sinilar to protein kinase pir||A57676; similar t
ESTs gp|A1993651.1, dbj|AV538995.1, dbj|AV522524.1, and
dbj|AV538995.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unknown protein; similar to EST emb|Z30724.1"
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GSTLLVYARSVCGNNINFYQIMPSRSHHAPGDLSYSFWESSHYHLFKLHRGTSALVCFDP
GFGLLVYARSTOGNINFYQIMPSRSHWAPGDLSYSFWESSHYHLFKLHRGTSALVQDI
CFGOGSQWA II ISKGTCH IF UNISGSSDAAPQPCEGEEPPRLPASSLPWMFTQSLS
NQQSLSPPTAVALSUVSRIKYSSFGMLNTVSNATTAATGKVFVPSGAVAAVFHKSVTH
KVEPTQWMDVCRRSDNLSTEERLPKSTTFEEPPRGTATAATGKVFVPSGAVAAVFHKSVTH
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INCHSRFGSIESAESSEGSTRQMENLIDSPHMSNIKSLFSLYPPRGTGSTR
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NLDDIIGAVFTPSYYEYSGRENEVENGKL
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VTFFGGEGGSKGIRLHCHCICOEFGAMOFLGSNAATAKTGKLIADPEPVWDREFFRFRH
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TPDAMAHITKSWYKALDYRFDLYNLHEJTESVWRTRLEFLKIRKGFGYONVCLACAM
SSYESLINDSLSKTTRLVQDARLENSEDYLSSWYDYVDVRPKRELEGGKLTITOWTR
FEMYETADFGWGKPVYAGPIDLRPTPQVCVLLPQGGVESGNDQSMVVCLCLPPAVHT
Submitted (15-JUL-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 101176) (benev, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chio, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Shantz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Direct, Submission
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/note="unknown protein; similar
/pb[721964.1, and contents similar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-JUL-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On Jul 15, 2000 this sequence version replaced 91:2618677. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
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complement(4838. .6223)
/note="hypothetical protein"
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Federspiel, N.A., Palan, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Hulzar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalaez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Tortiumi, M., Vyotskala, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
Submitted (30-JAN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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                                 Gaps
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                                                         2 CGTGATCGAAACGTGTAGAGTTGGGCCGCCGCCGCACTCGGTGGCGGAGCAATCGGTGCC
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    DB 12; Length 101176;
                                35;
                                Indels
                              0; Mismatches 692;
   Score 110.8; DB 1
Pred. No. 3.3e-16;
 7.58;
Query Match
Best Local Similarity 47.29
Matches 651; Conservative
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Federspiel, N.A., Fallm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Buh.M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B. I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

Lister Submission

Lister Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 119914)
Pederspiel,N.A., Falm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
Altafi.H., Araujo.R., Hulzar,L., Rowley,D., Buehler,E., Dunn,P.,
Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V.S.,
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                            38409 CCCATTATCCAACCTCAATTGCAGGAGCTCCGAAATTGGGACTGTATGACATGGATTTTG 38468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
CGCTTTGTAAAGCCAGGGA!TTTCGAAGGAGGATTGGAGGTTTGCTTGTTTTGCCTAAGG 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA PLN 30-JAN-1999 chromosome I BAC F21M11 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1294 ACAAAATGGATGCTTTTGC%GCTTATTTTTCACTGGGAATTAATGGTTAATAAATGTA 1351
                                                                                                                                                                                                                                                                                                                                                                                                      GATGGGGGAAGGCGAGAAAi3CAAGAAATATTGTCGATTGATGGGGGAAATATGCAATGA
                                                                                                           ACAAGAGAATATTAGAAACGGTGGAGAAATGGTCGCCGGAGATTCGTAAAGCGTTGCAGA
                                                                                                                                                                               GCGA - - - TCTGTTGAAGACAGCACCAAGATGGGGACAAGGAGTACGTAAATGGGTCATGT
                                                                                                                                                                                                                                                        AATCATATT - - - TTTCGGTGGCAGGATCGAGCTAGATCTTTACGGTGCAGATTTTG
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COMMENT

FEATURES

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.21994,
                                                                                                                                                                                                                                                                                                   /proteIn_id="Aad10667.1"

//broteIn_id="Aad10667.1"

//canslation="MLOGISSHTHERLSVETAEPHHLNDRVHIVEEIPKASVIPITE
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TOOLITEAASNSGSYPENHYKYKORESDDOLEEDEPCOSOSDLDEDEEYYSDYGFSE
DSLHNPTKRVTQDIGDKTEEIDSKLKRSNETVRDGNYTDGGVLROWKSAK
SKGRTKQKQSQKENSNFIADQEEKRDSSSFGTDDQITLSVKPKCRIEPKKLRNQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FESEYDAANHTPESTTEGAAKUVRDITASEQPSNAARKRICGESFIOESSPNEKTODP
TLERABESTERSDPPTDVYRAQNHQWYRSTEWUTSTSYLLCLRSNBLRCVYTEVQOLDK
SHTEQDSKRKRDITASDAMENHLKVPKRENNLAKOVTFCVQOLDK
SHTEQDSKRKRDITASDAMENHLKVPKRENNLAKOVTFCVQOLDK
KALEQTSSNITICGFCQSARVSEATGEMLHYSRGRPVDGDDIFRSNVIHVHSACIEWA
BOYY YEGDTYKNLKABELARGMAKIKCTKCSKCAAALGGFVRACRRSTHVPCAREISRCR
WDYSDPLLLCPAHSSYKFPURRKSGHRVSRABELDKINPACAEETSRCR
WDYSDPLLLCPAHSSYKFPURRKSGHRVSRABELDKINPACAEETSRCR
SALSKSDKKLMESLAVFRNRKSGHRVSRABELDKINPACHTELLUGG
SALSKSDKKLMESLAVFRNATISRYMNPSVTHVIASTDEKGACTRILKVLMGILNGKW
GDFYKGYKEDLQULYKVAGGTILLNTEDELGARSSNNVNDORSSSIVVYNIDPPHGGAL
GEEYTIIWQRANDAGALASOTSCRLVGHTWVLESIAGYKKHPPVIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAVDASĽSTWĽSTSESGSECNSASMYTLTPEKLKŠTSCYSKPLRINHDDRPVLCALŤL
EDIKQFSATSTPRKSPSKSPDETPIIGTVGGYWGNRSKAIDCGSASSFKGIPNTSSKY
REDKSVNWHSTPFEARLEKALNNIDK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"MGSSSPEARARAQVPSMILIFLEIICTVHVYTNRRKLNRDVLSA
NLNIPKRVTRRDLRFMESVISIYKSLNAAVSVHLPQLQIPNDCNYKNDALNNSNSPKH
GESEDSEMTDKDVSKRSGGTDSSSRDGSPLPTSEESDPRPKHQDWTEKQLSDHLLLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIPGFASTQLRAWSILDCPYTPLDFNPLDLVWLDTTKLLSAVNCWFKCMVLDPYNQTD
HPECKSRPDSGLSAITELDPGYITGPLSTVWKEWLKMCVEFGIEANAIVAVPYDWRLS
PTKLEERDLYFHKLKLTFETALKLRGGPSIVFAHSMGNNVFRYFLEWLRLEIAPKHYL
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DGTLEKALEDYDPDSKRMLHQLKKYVPFFYIRNIAHRSSLAGFLLXHDDPVRRPLTPW
ERPPIKNVFCIYGAHLKTFVGYYFAPSGKPYPDNWIITDIIYFTEGSLVSRSGTVVDG
NAGFITGDETVYYHGLSLWCKNWLGPKVNITMAPOILIGKIKQQPEHDGSDVHVELNVDH
HEHGSDIIANMTKAPRVKYITFYEDSESIPGKRTAVWELDKSGY"
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/db_xref="G1:4204287"
/translation="MGANSKSVTASFTVIAVFFLICGGRTAVEDETEFHGDYSKLSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(16835. 17185,17274. 17392,17491. 17656, 17795. 17885,17982. 18079,18175. 18361,18504. 18604, 18705. 19049,19134. 19349,19439. 19791,19862. 19967, 20188. 202338), /gene="F21M11.4" //note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KWLDQHIHAYFAVGAPLLGSVEAIKSTLSGVTFGLPVSEGTARLLSNSFASSLWLMPF
                                                                         complement(join(14567: .14641,14787. .15831,15906. .16006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jóin(20752. .20994,21362. .21497,21596. .21740,21825. .2.
22102. .22178,22542. .22758,22920. .23064,23343. .23442,
23599. .23693,24021. .24072,24227. .24298,24441. .24647)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Unknown protein; Location of ESTs 203124T7, gb|H76794 and 203124XP, gb|AA605510"
                                                                                                                                                                                          /note="Unknown protein; Location of ESTs 40C3TT, gb|AA728590 and40C3T7, gb|T04573"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Hypothetical protein"
       complement(14004. .16362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(16835. .20238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAD10669.1"
/db_xref="G1:4204288"
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/db_xref="G1:4204289"
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/gene="F21M11.6"
27777. .28734
/gene="F21M11.6"
28007. .28465
/gene="F21M11.6"
                                                                                                                16327. .16362))
/gene="F21M11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="F21M11.4"
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/gene="F21M11.5"
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                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                              e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described as
'putative', 'like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compblo.ornl.gov/section/index.html), GENSCAN (Chris Burge,
http://gnomic.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev
& A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and
NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MDRTMFLSLTIASLLVGVVSAGDWNILNOLRGLGSSSSONGIVS
KGIKKDLGKCKCENRINVEVHNIRKEDVVPGECSHIKDVEWISSOYKDDVARTVDEVI
LHFGSMCCSKSKCGMDAMPIEDIDTLLSTIPYHKKNGFFGGEKLNSTKFEDWIQKKR
APAVPHMKLYHDIRERGIKIFLISSRKEYLESATVDNLIQAGYYGNGNLMLAGLEDQ
QKEVKQYKSEKRKWLASLGYRVWGVMGDQMSSFAGCPLPRATFKLPNSIYYVA"
comptement (join(14004. 14312, 14565. 14641, 14787. 15831,
15906. 16006, 16327. 16382))
On Dec 30, 1998 this sequence version replaced g1:2734094.
Bases 1-9262 of clone F21M11 overlap with bases 6898-78259 of
"TAMU" BAC clone F20022 (Ac0002411) and bases 119525-119914 of clone
F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAYKULLDAIFDEADAQSTEKNKKEEEKKKREEEKKSRSVATSRGRRKAPEPLVQDEE
DDOEDDEFPLKRLLSRRGSRASSSSSSYRNEDLKYQFEEDEDGOVTELPPLKRY
VRRMGERGLAMTVARSPSSRLSMEDREPPPWTLLPAHPWETKYSEASALVILND
EPNIDHKPVISDTGNCSAPMLEMGKSNIHVQEWDWETKDILNDTTAMDVSPSSAIGES
SHRYNAASVELASSTSGEAKICLSFRANGFFTNIHLPSMEDLRRAMERCILKSYKI
VHPREVSVLGFWKDMSSYSJSGAKICLSFRANGFFTNIHLPSWEDLRRAMERCILKSYKI
VHPREVSVLGFWKDMSSYIDLARSTSOLLETETVOMSKAGDESGAVGISWPLVVVP
ECEISGDGWKAISNMKDITAGEENVEIPWVNEINEKVPSRFRYMPHSPYGDDAVIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAD10665.1"
/db_xref="GI:4204284"
/translation="MAPNLRIKKACDAMKLLGISETKTRAFLRKLLKTYENNWDFIEE
                                                                                                                                                                                                                                     as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Proteins in this region are annotated in the F21M11 entry, AC002411."
1. .9262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSSFSDEQSCSTSCIEDCLASEMSCNCAIGVDNGFAYTLDGLLKEEFLEARISEARDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKQVLRFCEECPLERAKKVEILEPCKGHLKRGAIKECWFKCGCTKRCGNRVVQRGMHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLQVFFTPNGKGWGLRTLEKLPKGAFICEYIGEILTIPELYQRSFEDKPTLPVILDAH
WGSEERLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="overlap with bases 68998-78259 of 'IGF' BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDIEAMEELAWDYGIDFNDNDSLMKPFDCLCGSRFCRNKKRSTKTMQILNKA"
join(13033. .13488,13717. .13926,14139. .14514)
/gene="F21M11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(7684. 7866,7965. 8027,8122. 8160,8250. 8381,8458. 8728,8875. 9833,10033. 10256,10344. 10410,10501. 10551,10685. 10781,10885. 10913)
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gene="Filml1.2"

/note="Similar to acid phosphatase; Location of ESTs

110c277, gb|142036, and 110c2xP, gb|A1100245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Hypothetical protein"
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/db_xref="G1:4204285"
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/chromosome="1"
/clone="F21M11"
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/gene="F21M11.1"
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/gene="F21M11.2"
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DNA
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JOURNAL
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SOURCE
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/translation="mntkTmrlPprrvlTadkrkErdafisSyTdnppElakFpSpPp
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KIRPSHTVEPAEECEPKRKRYREVANLLRSDGAQLPGIVNPAQLARFLKL"
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                                                                                                                                                                                                                       45957 TCATCGAGACCTGTCACATCTCTCCCCCAAAGGGCACCGTTCCATCAACCACTCTTCCTC 46016
                                                                                                                                                                                                                                                                                                                                      46617 TTTGGAGCCAAAACTCTGCAAAACACAGTTCACATGTTACGCCTGA-GAACATGGTCAGA 46675
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                                                                                                                                                                                                                                                                                    46017 TCACCTTCTTCGATGCCCCCTGGCTCTCTCTCCCCACTCGCCGATTCTCTTCTTCTTCTT 46076
                                                                                                                                                                                                                                                                                                                                                                                                                 46137 TCTCCATCACTCTCCAACATTTCTTCCCTTACGCCGGTAAACTGATTATCCCGCCTCGTC 46196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46676 GCCACTTTTACATTGAGCCGGAAGCAGATAGATAATCTAAAAAGTTGGGTTACAGAGCAG 46735
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                                                                                                                                                                                         63
                                                                                                                                                             Gaps
                                                             /gene="F21M11.7"
complement(join(29264. .31015,31312. .31414,31484.
31782. .32033))
                                                                                                                                                                                                                                                                                                                    124 AATTCCCTTGTTCCAAGCAACATTTTTCAGAATCCATCGTTCCAAAACTCAAACAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46736 TCTGAGAATCAATCTCCTGTTTCTACCTTCGTGGTGACTCTAGCTTTCATTTGGGGTAAGC
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                                                                                                                                                                                                                                                                                                                                                                                   TCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGATAGAA - - - AACTCT
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                                                                                                                          Length 119914;
                                                                                                                                                          Indels
                                                                                                                          Ouery Match 6.7%; Score 99.6; DB 12; Best Local Similarity 47.3%; Pred. No. 1.8e-13; Matches 657; Conservative 0; Mismatches 684;
                                              complement(29264. .32033)
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Fruit flavour related genes and use thereof Patent: WO 0032789-A 40 08-JUN-2000; AHARNI ASAPH (IL); VERHOEVEN HARRIE ADRIANUS (NL); LUECKER JOOST (NL); CPRO DLO (NL); CONNELL ANN PATRICIA O (NL); TUNEN ARJEN JOHANNES VAN (NL)
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ITLFPNQGFSIGVSSHHAILDGKTSTLFLKSWAYLCKQLQLCHHPCLSPELTPLLDRT
VIKDPTGQDMLQLNKWVVGSDNSDPQKIRSLKVLPFLDSESLNKLVRATFELTREDIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLRHKVNHOLSKSSKSKOVRLSTFVLTLAYVFVCMAKAKLAKAKTEAEAAAGNDEIKN
IIVGFTADYRSRLDPPIPLNYFGNCNGRHCETAKASDFVQENGVAFVAEMLSDMVKGI
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Sapindales; Rutaceae; Citrus.
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Aharoni,A., Verhoeven,H.A., Luecker,J., O'Connell,A.P. and
                                                                                                                                                                                                                                                                                                                                                   1164 GCAGATTTTGGATGGGGAAGGCGAAAAGCAAGAATATTGTCGATTGATGGGGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47210 GGITCIAICGCATICICAGAGICCAGAGACGGCAGCAAIGGAGITGAGATIGGAAIAGCA
46916 CCACAAACATACTTTGGCAACTGTATGGCTCCTGGTATCGTATCAGAAACACGAT
                                                                                                                                                 987 CTGGTGGGAGAAAGGGGTGTTTCTGGCAGCTGAGGTAATCGCGGGGGGAGATAAAAAA
                                                                                                                                                                                                                                                                                                           1047 AGGATCAACGACAAGAGAATATTAGAAACGGTGGAGAAATGGTCGCCGGAGATTCGTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47093 TGGGTCATGTCCCATTATCCAACCTCAATTGCAGGAGCTCCGAAATTGGGACTGTATGAC
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Address for correspondence: **cos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi/bin/adg_graph.cgi/c=MO01
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualiflers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
SplicePredictor (Volker Brendel, Stanford University,
http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://www.ini.achi.edu/chi.bin/sp.ggi).
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acyltransferase/benzoyltransferase-like protein"
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AYAYAWTCPYKARGGNRDRSVSLLFVGDFRDRLDPKLGGTVGCYNRKAAE
FMEEKGFVTAAEIISDLVKGLSSRKIETIADTFVEGFSFQSNSTQFGTIAGSTRLGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://gremlini.zool.lastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is Ti310 and the 3' clone is T26G12.
      Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC and BAC clones
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                                                                                                                                                                               2 (bases 1 to 85690)
Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
Direct Submission
                                                                                                                                                                                                                                                                    Submitted (09-JUN-1999) Yasukazu Nakamura, Kazusa DNA Research
                                                                                                                                                                                                                                                                                            Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2123. 8637
/note="contains similarity to TNP2-like transposon
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/note="contains similarity to unknown protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:3702"
                                                                                                                DNA Res. 7 (3), 217-221 (2000) 20363099
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Kaneko, T.,
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AISLAERRDGGGGVEVGVVLEKQQMEVFESVFADGLKNDLV"
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                                                                                                                                                                                                                                                                                                                                                      990 AGCTAAATTAGCCAAAGCCAAAACTGAAGCTGAAGCTGCAGCAGGTAATGATGAATTAA 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1168 GTTCAAGAAAATGGGGTTGCT-TTTGTTGCAGAGTGTTAAGTGATATGGTCAAAGGGAT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1112 GCAGAA-----ATCATATTTTCGGTGGCAGGATCGAGCAAGCTAGATCTTTACGGTGCA 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1287 CCTAAGGACAAAATGGATGCTTTTGCTGCTTATTTTTCACTGGGAATTAATGGTTAATAA 1346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1347 ATGTATGTAATTAAACTAATATTATTATGTAACAATTAAGTGTTGAGTGAACGTGAA 1406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1050 AAATATTATTGTGGGATTCACTGCGGATTATAGGAGCCGTTTGGATCCTCCAATTCCACT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1052 CAACGACAAGAATATTAGAAACGGTGGAGAAATGGTCGCCGGAGATTCGTAAAGCGTT 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1577 AAGAAATAAATTATTGCGGATTTTTGTGACCACCAAATAAAATACTCTTTTTTGAAAAA 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1227 CGATG--CGGATGCCATTGAAGCCAATGATGATAAGGTTTCAGAAATATTGGAAATTCTG 1284
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                                                                                                                                                                                                                                                                                                                                                                                                             872 GGATGCATTTTTTTTTTGATTCCGGTCGATCTAAGGCCACGATTAGATCCGCCGGTTCCTGA 931
                                                                                                                                                                                                                                                                                            812 AGCTTATATGTGGGCTGGCATAACGAAATCATTCACAGCAGATGAAGACCAAGACAACGA 871
                                                                                                                                                                                                                                            Gaps
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Pl clone:MOD1
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                                                                                                                                                                                                                                         18;
                                                                                                                                                                            Length 1648;
                                                                                                                                                                         Score 76.8; DB 9; Length 10
Pred. No. 3.4e-08;
0; Mismatches 312; Indels
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                                                         BASE COUNT
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AB028618
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VERSION
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 TCGAAGAATCCGATAGAAAGTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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complement(46109. .47990)
/note="contains similarity to reverse transcriptase
gene_id(MOD1.13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 GAAATCGTCCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTG
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                                                                                                                                                                                                                                             /evidence-not_experimental
complement(join(42135. .42706,42772. .43162))
//note-"gene_id:MoDl.11
unknown protein"
                  complement(join[40204. .40603,40656. .40872))
/note="gb|AAC97247.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
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LLLSTFVYTYEKSSGOSLFCKEEAKKSL"
                                                                                            gene_id:MOD1.10
similar to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental complement(52336. .56745)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene_id:NOD1.14
                                                                                                                                                                          /codon_start=1
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EBMQKELKAHRAEIVNVSKVLFRNPMAPKK"
2000plement(join(3460.33573,33657.34016,34094.34255,34330.3570,35486.35721,35799.36093,36146.36256))
                                                                                                                                                                                                                                                                       KLTESSRDSFFSSILPKLEGGLSLVLSHFLPLSGHLKWNPQDPKPHTVTFPKDTVSLT
VYBSEADESTSISKELRLEFELRPLVPELQYSDSASILLSCJTLFPRNGFSIGTTVH
HVVWGRTASKFHKSWAHICKHGTPROPEDTVLDRTVINVPAGLEGKIFGLSSYIS
EEKDYARTLTLPPAKEIDNDVVRVTLELTEVJIEKLKERAKNSSTRSDLHLSFFVVSY
                                                                                                                                                                                                                                                                                                                                                                                                                    AYVLTCMVKSCGGDANRPVRFMYAADFRNRLDPPVPLTYFGNCVLPIDFNGYKATTFL
GKDGYVNGVEILSDSVRGLGSRNIESIWEVYEDGTKNMKLDTQNVTVTGSNQFGIYGS
DFGWGRPVKTDVMSLYKNNEFSMSARRDEIGGLEIGISLKKCEMNVFLSLFTSDFDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"mrlagacrsspeeesrrrsrarawgsvdrpfiretyaadfrnrld
ppvplfyfgncvlptdfngyeattflgedgfvngveilsdsvkglgsrslesvwevye
Egtknmkvgtkvlfvtgsngfgixgadfgwgrpvntdvmslyknnsfsmsarrdeigv
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PVDFCVPTKPERELSFEARAGCORACKVPRKRIENBEKGFTLEDZIN
HVLGTTEVIESITEKAEKAEFEDENDVDKHDVVDSRMKRLGGGREIRFEEV
YNEDVQARMEAPNEEEVPTAVGPGDPTLVDVMEKLHSINDKLNEALLVLMEIEEKQAT
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PKLFQLLPYLSKEKVNARNLMLPPAKENINVVRVTLELSEANIKKLKEQAKNESTWSD
                                                                                                                                                                                                                                      /translation-"MALNVIKISRVSLVTNSVEPLVLPLTFFDLLWLKLNPIERVTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MPPKTRGGGGGKRNEIEASAPAKTEKVKAPAEKVKEGAPSKKAK
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complement(36608. .37000)
/note="gene_id:MOD1.9
                                                                                            /product-"anthocyanin 5-aromatic
acyltransferase/benzoyltransferase-like protein"
/protein.id="BAB02519.1"
/db_xref-"GI:11994478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(27960. .28438,28676. .28739))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Mutator-like transposase"
join(32547. .32726,32904. .33122)
/note="gene_id:MOD1.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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/db_xref="G1:11994479"
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/protein_id-"BAB02522.1"
/db_xref-"G1:11994481"
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/db_xref="GI:11994482"
                                                                  /evidence=not_experimental
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29217. .31674
/note="gene_id:MOD1.6"
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unknown protein"
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                                                                                                                                                                                                                                            TC-----ATTACCGACGGACGCATTCGAACCACGTTCGTTTTCACCCAATCCA 735
                                                                                                                                                                                                                                                                                                                                                       CTTTTGTAGCGATTGCAGCTTATATGTGGGCTGGCATAACGAAATCATTCACAGCAGATG 855
                                                                                                                                                                                      632 TGACTCCATTTATTGGA-----GAAACGCGCTAAAATTTCCTTTGCAATCTCGTCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16190 ATTTGGTGAAAGGGTTGAGTTCAAGAAAGATAGAGACCATTGCGGACACTTTCGTGGAAG
                         GCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTC
                                                                                                                                                                                                                                                                                                  AAATTAAGAAATTGAAGGGTTGGATTCAGTCCAGAGTTCCAAGTTTAGTCCATCTCTCAT
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                                                                             514 TCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACA--CATTGAAAATGAAGATGAAGA
                                                                                                                                  572 TGAAGAATTTAAATCTTTGCCAGTTTTCGATAGATCCGTCATAAAATATCCGACGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                916 ATCCGCCGGTTCCTGAAAATTACTTCGGGAACTGCTTATCGTACGCGCTGCCGAGAATGC
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15557 ATGACTCAGCGA-
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AC069470 136047 bp DNA HTG 19-JAN-2001 Arabidopsis thallana chromosome I clone IGF-F7F7, *** SEQUENCING IN PROGRESS ***, 4 unordered pleces.

DEFINITION

AC069470

ACCESSION

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicacea; Arabidopsis.

I (bases I to 136047)

Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Ronning,C.M., Koy,H., Fulli,C.Y., Utterback,T., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana 'IGF' BAC 'F7F7' genomic sequence near marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90161 AGCCAGTCAAAAGAGTCTTCTACGAGCTCACCGAGTCTACTCGTGACCATTCCACT 90220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCCCATGCTTCAGCTCCTCTTCTACGAATTCCCTTGTTCCAAGCAACATTTTTCAGAAT 156
                                                                                                                                                                                                                                                                                           Town, C.D. and Kaul, S.
Town, C.D. and Kaul, S.
Town, C.D. and Kaul, S.
Direct Submission
Submitted (01-30/10-2000) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
On Jan 19, 2001 this sequence version replaced gi:12280790.
* NOTE: This is a "vorking draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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Pred. No. 1.5e-07;
0; Mismatches 651;
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Arabidopsis thaliana
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Ronning,C.M., Roo,H., Fuli,C.Y., Utterback,T., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M., Arabidopsis thaliana 'IGF' BAC 'F7F7' genomic sequence near marker

GI:12320593

AC069470 AC069470.10

ACCESSION

VERSION

HTG; HTGS_PHASE1. thale cress. Arabidopsis thaliana

ORGANISM

KEYWORDS SOURCE REFERENCE AUTHORS Submitted (01-JUN-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr org no Jan 19, 2001 this sequence version replaced gi:12280790.

* NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

2 (bases 1 to 136047)
Town,C.D. and Kaul,S.
Direct Submission

AUTHORS TITLE JOURNAL

Unpublished

JOURNAL REFERENCE

TITLE

100163: contig of 100163 bp in length 100213: gap of unknown length 112623: contig of 12410 bp in length 112673: gap of unknown length 116686: contig of 3963 bp in length 116686: app of unknown length 116680: contig of 19361 bp in length 136047: contig of 19361 bp in length.

be preserved

/organism="Arabidopsis thaliana"

Location/Qualifiers

source

FEATURES

/db_xref="taxon:3702"

/chromosome="I" /clone="IGF-F7F7"

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                                1036 AGATAAAAAAAGGATCAACGACAAGAGAATATTAGAAACGGTGGAGAAATGGTCGCCGG 1095
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394 TCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAG 453
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                                                                      454 GCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTC
                                                                                                                                              514 TCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACA - CATTGAAAATGAAGATGAAGA
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                                                                                             Length 136047;
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  151 others
                                                                                             Score 68.8; DB 74;
Pred. No. 6.1e-06;
0; Mismatches 507;
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46028 a 22872 c 22213 g 44783 t
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Best Local Similarity 46.3%;
Matches 461; Conservative (
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AC069470 136047 bp DNA HTG 19-JAN-2001 Arabidopsis thaliana chromosome I clone IGF-F7F7, *** SEQUENCING IN

RESULT 14 AC069470/C LOCUS DEFINITION

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                              765 TCCAGAGTTCCAAGTTTAGTCCATCTCTTTTTTTTTTTGTAGCGATTGCAGCTTATATGTGG
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Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowloox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                     plants
tone,
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                                               DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
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                                                                                    Claim 4; Page 65-69; 94pp; Japanese
Fukui Y,
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99.9%; F
Ashikari T, Fujiwara H, Fuk
Nakao M, Tanaka Y, Yonekura
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Best Local Similarity 99.9
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                                                                                                                                                                                                                                                                    Mizutani
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               /*tag= a
/product= Aromatic acyl transferase.
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                                                                                                                                                                                                                                                                    Kusumi T,
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 73-76; 94pp; Japanese.
                                                                                                                                                                                                                                                                    Fukui
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Nakao M, Tanaka Y, Yonekura K;
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95JP-0196915.
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29-JUN-1995;
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                                                                                                                                                                                                                                                                      Aromatic acyl transferase; transformation; anthocyanin pigment; plante; colourtation; colour change; celouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= Aromatic acyl transferase.
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Tanaka Y, Yonekura K;
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/transl_except= ATC encodes
1322..1324
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                                                                                    AAT37309 standard; cDNA to mRNA; 1622
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14.7%; Score 216.8; DB 17; Length 1622; llarity 50.8%; Pred. No. 5.7e-47; Conservative 0; Mismatches 662; Indels 57;

Similarity

Query Match Best Local Simi Matches 741;

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tone,
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                                                                                                                           1259 gigcaigaittigaigcagaittiggitggggaaagciigaaaagcaigaaictgiitca
                                                         ATTGATGGGGAGAAATATGCAATGACGCTTTGTAAAGCCAGGGATTTCGAAGGAGGATTG
                                                                                          GAGGTTTGCTTGTCTTTGCCTAAGGACAAATGGATGCTTTTGCTGCTTATTTTCACTG
                        CTAGATCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAAGCAAGAAATATTGTCG
                                                                                                                                                                                                                                                                                        Aromatic acyl transferase; transformation; anthocyanin pigment; plante; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coding for aromatic acyl transferase - for transforming ch produce anthocyanin pigments and thus altering colour of flowers
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/product= Aromatic acyl transferase.
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..... M, Tanaka Y, Yonekura
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95JP-0067159.
95JP-0196915.
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P-PSDB; AAW04726.
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17-FEB-1995;
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                                                                                                                                                                                                               Length 1508;
                                                                                                                                                                                                                                                                  0; Mismatches 654; Indels
                                                                                                                                     BP; 442 A; 294 C; 295 G; 477 T; 0 other;
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                                            tggtaactgtggtgcaccatgtgtcccgaccttaaaaaatgtcgttttgactagcgaaaa 1018
                                                                                                                                                                       GAAGGCGAGAAAGCAAGAATATTGTCGATTGATGGGGAGAAATATGCAATGACGCTTTG 1240
                                                                                                                                                                                 TAAAGCCAGGGATTTCGAAGGAGTTGGAGGTTTGCTTGTCTTTGCCTAAGGACAAAAT 1300
                                                                                                                                                                                                                            tgcaagcaaaacatcagcacaagatcttgaaattggattgagtctaccgagtatgcaaat 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA coding for aromatic acyl transferase - for transforming plants
1001 AGGGGTGTTTCTGGCAGCTGAGGTAATCGCGGCGGAGATAAAAAAAGGATCAACGACAA
                                                                                1019 tgggtatgcacttggtgctaaagtaattggagagtctatatgcaaaatgatatataaaa
                                                                                                                   ggacggaatcttgaaagatgccgcgagatggcatga---acctttcatgatcccggctag
                                                                                                                                                     CGGGAACTGCTTATCGTACGCGCTGCCGAGAATGCGGCGGCGGCGAGAGCTGGTGGGGAGAGAA
                                                                                                  GAGAATATTAGAAACGGTGGAGAAATGGTCGCCGGAGATTCGTAAAGCGTTGCAGAAATC
                                                                                                                                    1121 ATATTTTCGGTGGCAGGATCGAGCAAGCTAGATCTTTACGGTGCAGATTTTGGATGGG
                                                                                                                                                                                                                                                                                                                                                                                Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; scenecio cruentus; Lavandula angustifolia; ds.
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                                                                                                                                                                                                                                             GGATGCTTTTGCTGCTTATTTTCACTGGGAATTAATGGTTAA 1343
                                                                                                                                                                                                                                                       /product- Aromatic acyl transferase
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gentiana triflora var. japonica (Clone pGAT4)
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                                                                                                                                                                                                                                                                                                                                                                Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                                                           BP.
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ura K;
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95JP-0067159.
95JP-0196915.
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                                                                                                                                                                                                                                                                                                          AAT37308 standard;
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17-FEB-1995;
29-JUN-1995;
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                                                                                                                                                                                                                     with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                             Vectors containing DNA fragments encoding proteins of plant origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCTACCCTTCATCCCCGGAGAAAATGCCGGAGTTTCGGTA-----TCTATCCGGGGAC
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which produce anthocyanin pigments and thus altering colour tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17; Length 1703;
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llarity 49.6%; Pred. No. 3.8e-36;
Conservative 0; Mismatches 666;
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                                                                                                              Claim 4; Page 53-57; 94pp; Japanese
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es 703; Conserv
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                                                                                               GCGCCGGAGATAAAAAAAAGGAT---CAACGACAAGAGAATATTAGAAACGGTGGAGAAA 1085
                                                                                                                                                    TGGTCGCCGGAGATTCGTAAAGCGTTGCAGAAATCATATTTTTCGGTGGCAGGATCGAGC 1145
                                                                                                                                                                                    AAGCTAGATCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAAGCAAGAAATATTG 1205
                                                                                                                                                                                                                              1392 gaaggettttgetetttgteatagtetetttaatagaaceatatttgetgeaataagta 1451
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ggagaagccattgaaaagaggttgcacaacgaaaaaggcgttcttgcagatgcaaaaact
                                                                                                                                                                TCGATTGATGGGGAGAAATATGCAATGACGCTTTGTAAAGCCAGGGATTTCGAAGGAGGA
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                       ------ACCAAGACAACGAGGATGCATTTTTTTTTCTTGATTCCGGTCGATCTAAGGCCA
                                      gaatcatcgaacgaaaaatgagctcgagtacttcagttttacagcggattgccgagga
                                                      CGATTAGATCCGCCGGTTCCTGAAAATTACTTCGGGAACTGCTTATCGTACGCGCTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                          AAF58252 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               имимимимимимимимимимимимимимимимитадесимимимимимимимими 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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1 Similarity 7.1%; Pred. No. 3.5e-15;
36; Conservative 284; Mismatches 186;
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                                                                                                                                                                                                                                                                                                                                                           974 GCGCCGCCGAGAGCTGGTGGAGAGAGAAAGGGGTGTTTCTGGCAGCTGAGGTAATCGCGGC 1033
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                                                                                         (CLIN-) CLINICAL MICRO SENSORS INC
                                       26-JUL-2000; 2000WO-US20476
                                                           26-JUL-1999; 990S-0145695
17-MAR-2000; 2000US-0190259
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WO200107665-A2
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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ilarity 7.1%; Pred. No. 3.5e-15;
Conservative 284; Mismatches 186;
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                            BP
AAF58257/c
ID AAF58257 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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                                                                                AAF58257;
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TTGCTTGTCTTTGCCTAAGGACAAAATGGATGCTTTTGCTGCTTATTTTCACTGGGAAT 1333
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                          TCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAGCAAGAAATATTGTCGATTGA 1213
The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                             TGGGGAGAAATATGCAATGACGCTTTGTAAAGCCAGGGATTTCGAAGGAGGATTGGAGGT
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17-MAR-2000;
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TGAGTAACGTGAAGAATAATCCCTATTATATATTTTATGATTTGGTTCAAATAAAGTGTAA 1453
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                                                                                                     1454 AGCCTCTTGAAAAAAAAAAAAAAA 1479
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2000US-0190259
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17-MAR-2000;
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                                                                                                                           TCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAAGCAAGAAATATTGTCGATTGA 1213
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 DB 22; Length 936;
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6.4%; Score 94.8; DB 22;
ilarity 7.1%; Pred. No. 3.5e-15;
Conservative 284; Mismatches 186;
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                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                                                                                                                                                                                                                               6.4%; Score 94.8; DB 22;
ilarity 7.1%; Pred. No. 3.5e-15;
Conservative 284; Mismatches 186;
                                                                                                                                                                                                                                                             Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
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Example 6; Page 127; 159pp; English.
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ATTAATTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTATATATTTATGATTTGGTTC 1440
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two nucleic
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Pred. No. 3.4e-14;
00; Mismatches 305; Indels
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                                                                                                                                                                                      Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                                                                                                                                                               Example 6; Page 127; 159pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Page 127; 159pp; English.
                                                                                                                                                       (CLIN-) CLINICAL MICRO SENSORS INC
      26-JUL-2000; 2000WO-US20476.
                                                           26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monitoring gene expression.
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TAAGGCCACGATTAGATCCGCCGGTTCCTGAAAATTACTTCGGGAACTGCTTATCGTACG
                                                                                                                    CGCTGCCGAGAATGCGGCGGCGAGAGCTGGTGGGAGAAAAGGGGGTGTTTCTGGCAGCTG
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                                                        Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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                                                                        The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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Conservative 450; Mismatches 305;
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Pred. No. 3.4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901 TAAGGCCACGATTAGATCCGCCGGTTCCTGAAATTACTTCGGGAACTGCTTATCGTACG 960
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Best Local Similarity 0.5%; Pred. No. 3.4e-14;
Matches 4; Conservative 450; Mismatches 305; Indels
                                                                                                                    Electron-transfer group; ETM; mismatch; genotyping;
gene expression; ss.
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                                                                                                                                                                                                                                                                                                        (CLIN-) CLINICAL MICRO SENSORS INC.
               AAF58259 standard; DNA; 936 BP
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17-MAR-2000; 2000US-0190259
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                                                                                          Oligonucleotide D2004
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
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US-08-232-463-14
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1659.305 Million cell updates/sec
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Sequence 186, App
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Sequence 14, Appl
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Sequence 27, Appl
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                                                                                                                                            ; Search time 168.74 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-913-842-20
US-08-913-842-27
US-08-913-842-1
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US-08-913-842-2
                                                                                                                                                                                                          324599 segs, 94655562 residues
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                                                                     5, 2001, 18:04:28
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             nucleic search, using sw model
                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA:*
                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
                                                                                                                     US-08-894-356C-4
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Query
Match Length D
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Maximum DB
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 288, App
Sequence 487, App
Sequence 1, Appli
Sequence 5, Appli
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-FIOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-08-242-677-1

US-08-446-855A-1

US-09-150-741-1

US-08-150-741-1

US-08-102-033-1

US-08-998-416-288

US-08-998-416-288

US-08-998-416-288

US-08-391-1

US-08-391-1

US-08-101-1

US-08-101-1

US-08-101-1

US-08-144-815-5

US-08-444-813-5

US-08-444-813-5

US-08-444-813-5
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FATKNER, F. 5.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 394768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                   ; Sequence 14, Application US/08232463
; Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                        Foley & Laxdner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703)836-9300
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COUNTRY:
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                                                                                                982 GAGAGCTGGTGGGAGAGAAAGGGGTGTTTCTGGCAGCTGAGGTAATCGCGGCGGAGATAA 1041
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                                                                                                                                                                                                                                                                                                                                 1102 GTAAAGCGTTGCAGAAATCATATTTTCGGTGGCAGGATCGAGCAAGCTAGATCTTTACG 1161
                                                                                                                                                                                                                                                                                                                                                                                                                1162 GTGCAGATTTTGGATGGGGGAAGGCGAGAAAGCAAGAAATATTGTCGATTGATGGGGGAGA 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              922 CGGTTCCTGAAAATTACTTCGGGAACTGCTTATCGTACGCGCTGCCGAGAATGCGGCGGC 981
                                                                            862 AAGACAACGAGGATGCATTTTTTTTGATTCCGGTCGATCTAAGGCCACGATTAGATCCGC 921
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4.4%; Score 65.8; DB 1; Length 7218;
Best Local Similarity 7.5%; Pred. No. 9.7e-10;
Matches 31; Conservative 219; Mismatches 161; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-AUG-1991
ATTORNEY_AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FO
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LATGHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 91 114
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-232-463-14
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INSECT-SPECIFIC PARALYTIC NEUROTOXIN
GENES FOR USE IN BIOLOGICAL INSECT CONTROL: METHODS AND
COMPOSITIONS
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                                                                                                                                                                                                                       Length 7218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/593,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Greenlee and Winner, P.C. STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/07593657; Patent No. 5266317; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tomalski, Michael D. APPLICANT: Miller, Lois K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ferber, Donna M. REGISTRATION NUMBER: 33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                  LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: INSETITLE OF INVENTION: GENETITLE OF INVENTION: COMPONER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSE: Greenlee an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19901004
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US-08-232-463-14
                                                                                       linear
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                                                                                       TOPOLOGY:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 ATTTTTAAATTAGTAAATTTCGATAATTTTACTTAATTTTTTAAATTTACTAAATTGAC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 186, Application US/08998416
Fatent No. 6239264
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Polliman, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mont, Christine
APPLICANT: Mont, Christingle Park
STREET: 3054 Cornwallis Road
CITY: Month, Christingle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                               Query Match 2.9%; Score 42.6; DB 1; Length 319; Best Local Similarity 52.5%; Pred. No. 0.0016; Matches 93; Conservative 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PACENTIN PC-POS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNE: AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
REFERENCE/DOCKET NUMBER: 14-90
               TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
TELEPAX: 303/499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 base palrs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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TELEPHONE: 919-541-8587
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INFORMATION FOR SEQ ID NO: 186:
                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA

US-07-593-657-14
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US-08-998-416-186
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1356 ATTAAACTAATATTATTATGTAACAATTAATTAAGTGTTGAGTAACGTGAAGAATAATCC 1415
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APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Wohl, Christine
APPLICANT: Wondland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Respischung, Corinne
APPLICANT: Rebischung, Corinne
APPLICANT: Rebischung, Corinne
APPLICANT: Rebischung, SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       Query Match 2.8%; Score 41.6; DB 4; Length 615; Best Local Similarity 51.6%; Pred. No. 0.0049; Matches 95; Conservative 0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
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REGISTRATION NUMBER: 38,241
REPERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-541-858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 6239264artis Corporation
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; Patent No. 6239264
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-19:96
ATTONNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1074RP
US-08-998-416-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                      TYPE: nuclei
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919-541-8689
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                                                                                                                                                                                                                                                                                                                                                                                                      187 AAAA 190
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                                                                                                                     ; ORGANISM:
US-08-998-416-288
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  TELEFAX:
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0
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Pred. No. 0.0051;
0; Mismatches 89; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38.241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUTRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
  1137:
                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                        2.8%;
            SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                      Query Match 2.8'
Best Local Similarity 51.6'
Matches 95; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                    ; ORGANISM: PAG1692RP
US-08-998-416-1137
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US-08-998-416-288
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GENERAL INFORMATION:
APPLICANT: Tomalski, Michael D.
APPLICANT: Miller, Lois K.
TITLE OF INVENTION: INSECT-SPECIFIC PARALYTIC NEUROTOXIN
TITLE OF INVENTION: GENES FOR USE IN BIOLOGICAL INSECT CONTROL: METHODS AND
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                1356 ATTAAACTAATATTATTATGTAACAATTAATTAAGTGTTGAGTAACGTGAAGAATAATCC 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                Length 837;
                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                Score 41.6; DB 4;
Pred. No. 0.0061;
0; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greenlee and Winner, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          us/07/593,657
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: Patent No. 5266317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 303/499-8080
                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                  2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1241 base pairs
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.69
Watches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US
FILING DATE: 19901004
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 303/499-808
TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                 PAG1241RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID STRANDEDNESS: doub
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Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Peterson, David H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin.zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ENTHROCYTE BINDING PROTEINS
 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                       3: Knobbe Martens Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38.6; DB
Pred. No. 0.41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORREY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1451 TAAAGCCTCTTGAAAAAAAAAAAAAAAA 1479
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FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy cisk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 235-3550
TELEFAX: (619) 235-0176
INFORMATION FOR SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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ADDRESSEE: Knobbe Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92660
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 80; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                      RESULT 9
US-08-487-826B-13
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Patent No. 633528
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Muller, Lois K.
APPLICANT: Dia Albert
APPLICANT: Dia Albert
APPLICANT: Black, Peter
APPLICANT: Black, Bruce
TITLE OF INVENTION: Biological Insect Control Agents Expressing
TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and Compositions
FILE REFERENCE: 28-96a
CURRENT FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: 08/729,606
PRIOR FILING DATE: 2000-10-01
                                                                                                                                                                                                                                                                                                                                                              1056 attittaaattagtaaaatticgataattitacitaattititaaattiactaaatigac 1115
                                                                                                                                                                                                                                                                                                                                           1363 TAATATTATGTAACAATTAAGTGTGTGGGTAACGTGAAGAATAATCCCTATTAT 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1363 TAATATTATTATGTAACAATTAATTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTAT 1422
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                                                                                                                                                                                                                                                              Score 39.4; DB 1; Length 1241; Pred. No. 0.037; 0; Mismatches 86; Indels 0
                 MOLECULE TYPE: CDNA to mRNA FEATURE:
                                                                                                                                                                                                                                                              Query Match 2.7%;
Best Local Similarity 51.4%;
Matches 91; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Ver. 2.0
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                                                                                                             unsure
-103..-100
                                                      CDS
119..985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: CDS
; LOCATION: (119)..(985)
US-08-942-0128-3
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                                                                                                                                                                    unsure
47..49
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SEQ ID NO 3
LENGTH: 1241
                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                ; NAME/KEY;
; LOCATION:
US-07-593-657-6
TOPOLOGY:
                                                      NAME/KEY:
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US-08-942-012B-3
                                                                        LOCATION:
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                                                                                            FEATURE:
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Length 19124;
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20.08-916-443A-16
Sequence 16, Application US/08916443A
Patent No. 6001986
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20889-5606
                                            Maryland
    STREET: Bldg 1
CITY: Bethesda
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                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                              TITLE OF INVENTION: Antiviral Proteins, Amarandin 1 and 2, from TITLE OF INVENTION: Amaranthus Viridis, DNAs Encoding Therefrom NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 36.4; DB 3; Length 1116; 55.6%; Pred. No. 0.29;
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Patent No. 5814617
GENERAL INFORMATION:
APPLICANT: Charoenvit, Yupin
APPLICANT: Hedstrom, Richard C.
APPLICANT: Description Richard C.
TITLE OF INVENTION: Protective 17 kDa Malaria Hepatic and TITLE OF INVENTION: Erythrocytic Stage Immunogen and Gene NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/916,443A
FILING DATE: 22 AUG 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 1942/18
REFERENCE/DOCKET NUMBER: 1942/18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEPHONE: 202-429-1776
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                3+ Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1116 nucleic acids
                APPLICANT: Sun Chung PARK APPLICANT: Soo Kyung OH APPLICANT: Hosull LEE APPLICANT: Jeong Woo CHO APPLICANT: Chang H. CHUNG
Yong Sig KIM
Sun Chung PARK
Soo Kyung OH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 55.6
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Flop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleotides
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                                                                                                                                                                                                                                                                                      20036
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US-08-319-704-5
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1265 ATTGGAGGTTTGCTTGTCTTTGCCTAAGGACAAAATGGATGCTTTTGCTGCTTATTTTC 1324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1385 ATTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTATATATTTATGATTTGGTTCAAAT 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 ATAGCATAGATTATCTCTATATAGAAAAAATATTAAAAAAATATTTTTATAATCTTT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Whoriskey, Susan K.
APPLICANT: Whoriskey, Susan K.
APPLICANT: Quinn, Cheryl L.
APPLICANT: Touinn, Cheryl L.
APPLICANT: Politis-Virk, Karen I.
APPLICANT: Schimmel, Paul R.
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: Synthetase Genes, Tester Strains and Assays NUMBER OF SEQUENCES: 4
CORRESPONDENCE: 4
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.4; DB 1;
Pred. No. 0.34;
0; Mismatches 111;
8: Naval Medical R & D Command
Bldg 1, T-12, 8901 Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1445 AAAGTGTAAAGCCTCTTGAAAAAAAAAAAAAA 1478
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                                                                                                                                                                                                                                                                                                                                                                             ATORNEY/AGENT INFORMATION:
NAME: A. David Spewack
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: 75,206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-1022
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1422 base pairs
TYPE: nucleic acid
STRANDEDNESSÉ: single
                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,704
FILLING DATE: 07-0CT-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 40, Application US/08415593
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA (genomic)
US-08-319-704-5
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Best Local Similarity 48.1%;
Matches 103; Conservative C
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CITY: Lexington
...R: Massachusetts
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; Patent No. 5912140 5776726
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1274 TIGCTIGTCTTTGCCTAAGGACAAATGGATGCTTTTGCTGCTTATTTTCACTGGGAAT 1333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1334 TAATGGTTAATAAATGTAYGTAATTAAACTAATATTATTATTATAACAATTAATTAAGTGT 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1970 ITTGCATATATTTTTGAAAAAAATTAAACAAATTTGTATTATAAAATGATTAAAATT 2029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1394 TGAGTAACGTGAAGAATANTCCCTATTATATTTTATGATTTGGTTCAAATAAAGTGTAA 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2030 ACTTAAAATATAAAAAGTGATTATTTTAAAGTTATAAATTCTTGTAAAATAATG 2089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PYTE, Anna M.
APPLICANT: PYTE, Anna M.
TITLE OF INVENTION: MUCTIPLE COMPONENT RNA CATALYSTS AND TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.5%; Score 36.4; DB 2; Length 2. Best Local Similarity 48.5%; Pred. No. 0.45; Matches 100; Conservative 0; Mismatches 106; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Cooper and Dunham, LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US,'08/378, 235B FILING DATE: 25-JAN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1454 AGCCTCTTGAAAAAAAAAAAAAAAA 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2090 TATGTATTTAAAAAAAAAAAAAAA 2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-415-593-39
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Sequence 8, Application US/08378235B

Patent No. 5872241

GENERAL INFORMATION:
                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION UNDBER: 22,592
REFERENCE/DOCKET UNDBER: CP194
TELECOMMUNICATION INFORMATION:
TELEFRAN: 617-861-6240
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2128 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1274 TTGCTTGTCTTTGCCTAAGGACAAAATGGATGCTTTTGCTGCTTATTTTCACTGGGAAT 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Whoriskey, Susan K.
APPLICANT: Whoriskey, Susan K.
APPLICANT: Quinn, Cheryl L.
APPLICANT: Too, Niajun
APPLICANT: Schimmel, Paul R.
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: Synthetase Genes, Tester Strains and Assays NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brock, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1991;
                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
2.5%; Score 36.4; DB 2;
Best Local Similarity 48.5%; Pred. No. 0.43;
Matches 100; Conservative 0; Mismatches 106;
                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
ATTONELY/AGENT INFORMATION:
NAME: BLOOK, DAVIG E.
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
RECEPHONE: 617-861-6240
ITELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1991 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1454 AGCCTCTTGAAAAAAAAAAAAAA 1479
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Patent No. 5912140
Patent No. 5912140 5776726
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CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
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; LOCATION: 29..1780
US-08-415-593-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-08-415-593-39
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STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                Query Match 2.4%; Score 36; DB 2; Length 174; Best Local Similarity 58.3%; Pred. No. 0.11; Matches 63; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1403 TGAAGAATAATCCCTATTATATTTATGATTTGGTTCAAATAAAGTG 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                   28,678
ER: 0575/45553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 0575,
TELECOMMUNICATION INFORMATION:
TELEPAN: 212-278-0400
TELEPAN: 212-291-0525
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: RNA (genomic)

US-08-378-235B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                        LENGTH: 174 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: PA
COUNTRY: US
ZIP: 19103
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US-07-867-106-2
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                                                                                                                                                                             1372 TATGTAACAATTAATTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTATATTTATG 1431
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                             ;
                                                                                                    Length 5852;
                                                                                                                                                                                                                                                                                                         Score 36; DB 1; Length 585
Pred. No. 1.2;
0; Mismatches 120; Indels
                                                                                                   Query Match 2.4%;
Best Local Similarity 47.4%;
Matches 108; Conservative
CDS
2378..5038
                                     CDS
2378..5038
NAME/KEY:
LOCATION:
                                      NAME/KEY:
                                                  ; LOCATION:
US-07-867-106-2
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Search completed: November 5, 2001, 18:04:45 Job time: 15085 sec

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2403.520 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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em_estroll:*
em_estroll:*
em_estro23:*
em_estro23:*
em_htc:*
gb_estl07:*
gb_estl09:*
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gb_gss13:*
gb_gss14:*
gb_gss15:*
gb_gss15:*

gb_gss11:* gb_gss12:*

4:8886_dg gb_gss10:

. jssb_db gb_gss9:

gb_gss17:* gb_gss18:* gb_gss19:*

gb_gss20:* gb_gss21:* gb_gss22:* gb_gss24:*

gb_gss23 gb_gss25

em_gss_rod2: *
em_gss_rod3: *
em_gss_rod5: *
em_gss_rot1: *
em_gss_vrt1: *
em_gss_vrt2: *
em_gss_vrt2: *

gb_gss3:* gb_gss4:* gb_gss5:*

gb_gss2:*

em_gss_rod1:

em_gss_pro:

em_gss_inv1:*
em_gss_inv2:*
em_gss_inv3:* em_gss_other:* em_gss_pln1:* em_gss_pln2:*

em_gss_hum7: em_gss_hum8: em_gss_hum5 ew_gss_hume

em_gss_hum9

em_gss_hum3:* em_gss_hum4:* em_gss_huml:* em_gss_hum2:*

gb_est110:*
gb_est111:*
gb_htc:* em_gss_fun:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_inv4: em_gss_rod6: em_gss_rod7: em_gss_rod8: gb_gss35:* gb_gss36:* gb_gss37:*

gb_gss31:*

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gb_gss30: gb_gss32 gb_gss34:

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ä 77 GTGAAGTTGGTCCACCACCACCACGTCCCTCAACCACCCTTCCCTGACTTTCTTCG 136 76 ACATGACGTGCCTTTTTCATCCCATGCTTCAGCTCCTTTTTACGAATTCCCTTGTT 135 9.4%; Score 139.4; DB 111; Length 687; 52.6%; Pred. No. 2.4e-25; ative 0; Mismatches 286; Indels 3; Gaps 16 GTAGAGTIGGGCCGCCGCCGCACTCGGTGGCGGAGCAATCGGTGCCGCTCACATTCTTCG 75

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1 (bases 1 to 690)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougit, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries Division tell 1.800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG599447 690 bp mRNA EST 12-APR-2001
EST504342 cSTS Solanum tuberosum cDNA clone cSTS25122 5' sequence,
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ATATTCCATGGTTCTACTGCCACCCCATCCACGCATCTTCTTCTATGACTTTCCCCACC 196
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                              CTCACATAGGCTACCTTGATGGAGACTCTCTCTCTTCACCGTTGCAGAGTCCACCGCAG
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                                                                                                                                                                                                                                                             ACTICACCCTCCTCACATCAGATTCACCACAAAGACGTTCCAAATTGGCACCCTCTTGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617 AAGGAAACATGGCTTNNCTTTCAACCTCTNTGTCTTTTTTTTTCTTGAGGGACAAAG
                                                                                               TCATACACTTCTTCCCTCTCTCTCATGCAATTTAATCTACCCTTCATCCCGGGAGAAAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Solanum tuberosum"
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/db_xref="taxon:4113"
/clone="cSTS25122"
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Solanum tuberosum
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TTAAAGATCC 686
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XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                 Score 131.8; DB 155; Lengt
Pred. No. 2.2e-23;
0; Mismatches 262; Indels
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546 GGAGATGAACA 556
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                                                                                                                                                                                                                                                                  /tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLM"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; cLEF - Fruit were tagged at the lcm stage and
harvested 3-5 days prior to ripening. Fruit were cut in
half to verify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 113; Length 606;
                                                                                                                                                                               /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xxef="Lengan-4081"
/clone="cleF9F1"
/clone="libe"tomato fruit mature green, TAMU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.9%; Score 131.4; DB 113; Lengt
Best Local Similarity 52.0%; Pred. No. 2.8e-23;
Matches 294; Conservative 0; Mismatches 271; Indels
          Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                SC 29634, USA
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                                                                                                                                 prime sequence.
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/tissue_trype="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post_inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR" each of these stages."
/note="vector: pBluescript Sx: site_1: ECORI: Site_2:
XhoI: cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post_inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Glapapek III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

219 c 97 g 236 t
                                                                                                                                                                                         Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Medicago truncatula/Glomus versiforme mixed EST library
1 (bases 1 to 783)
1 (bases 1 to 783)
1 Harrison, M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
BSTs from roots of Medicago truncatula after colonization with
Glomus versiforme, 2001
Unpublished (2001)
Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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EST486469 MHAM Medicago truncatula/Glomus versiforme mixed EST
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Noble EST name: N380179e TIGR sequence name: MTDBT67TK More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA qAA CTA qtg qAT CC).
Location/Qualifiers
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Pred. No. 4.2e-23;
0; Mismatches 277; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Medicago truncatula genotype A17" /db_xref="taxon:119092"
                                                                 ibrary cDNA clone pMHAM-19K14 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="pMHAM-19K14"
/clone_lib="MHAM"
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53.3%;
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Matches 323; Conservative
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Length 570;

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8.8%;
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1 (bases 1 to 583)
                                    Conservative
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                 Similarity
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                   Best Local Sim
Matches 282;
   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
(bases I to 570)

van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning
Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE922784 570 bp mRNA EST 02-0CT-2000 EST426553 potato leaves and petioles Solanum tuberosum cDNA clone cSTB22E2 5' sequence, mRNA sequence.
                                                                                                  Contact: Cathy Rouning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
                                               249 AATTCCCAAAACACCGATCCTTACATACGTTACCTCGATGAAGACTCTATCTCCTTCACC 308
                                                                                  ATCGCAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCCGTT 356
                                                                                                                                                                                                                                                                                                                                                          TCAATGAGCAAACACATTGAAAATGAAGATGAAGATGAAGAATTTAAATCTTTGCCAGTT 596
                                                                                                                                                                                                                                                                                                                                                                                    549 TCTCTTTCAAAAGCCATAGCAAAAACAACAATAATTTGTCTCTTGAATACTCTCGGCCT 608
                                                                                                                                                                                                                                                                                                               AGTTACAACCATGTTGCTGCAGACGGAAAATCACTTCACCATTTCGTGAAATTTTGGGCC
                                                                                                                                                                                    369 TGGCACCATCTTGTTCCAAATTTACCTCCACCTCGTACCGAACAAGACAACTCGCATC
               417 TTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGAATA
                                                                                                                                                                                                                                                                                         GCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCGTTTATAACGGCTTGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lip="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Solanum tuberosum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB22E2"
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae, Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                      121 ACGAATTCCCTTGTTCCAAGCAACATTTTTCAGAATCCATCGTTCCAAAACTCAAAAAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CTCTCTCTAAAACTCTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTACCCTTCAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 CACTCTCCCTCACTCTCAAACACTATACGCCCTTAGCTGGAAACGTTGCTCGTCCACTAG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 ATACAAACGGATATCCTGAGTTACATTATGTGACAGAGAGATTCTGTATCTGTATCTTTT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGATAGAAACTCTTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AAGTITICGCCGTGCAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGAATAGCAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGTCTTAGCCATTCAAGTGACACTTTTTCCGAATCTTGGTGTATCCATTGGTTTCACTA 510
                                                                                                                                                                                                                                    CGCTCACATTCTTCGACATGACGTGGCTGCATTTTCATCCCATGCTTCAGCTCCTTCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 CAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCCGGTAGGC 360
                                                                                                                                              1 CCGTGATCGAAACGTGTAGAGTTGGGCCGCCGCGGACTCGGTGGCGGAGCAATCGGTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 CGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCGTTTATAACGGCTTGGTCT 536
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  DB 142;
                                                        254;
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
Score 129.6; DI
Pred. No. 8e-23
                                                     0; Mismatches
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BASE CO ORIGIN

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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Whole plants were challenged with 450,000
sporanja'ml P. infestens US-1(US 940501) in Blotron
(Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid
nitrogen immediately upon removal. Kennebec plants showed
no signs of HR. Katahdin plants (susceptible to P.
infestens US-1) were used as controls and showed
infection, NOTE: We cannot exclude the possibility that
this sequence is actually derived from Phytophthora rather
than potato."
                                  I (bases I to (bases)

I hand, P. Hernandez, M. Tornqvist, C.-E, Wirtz, U., Loukolanov, A.,

Rangel, P., Haberlach, G.T., Cho, J., Chiemingo, A., Bougri, O., Buell
, C.R., Ronning, C.M., Helgeson, J. and Baker, B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Incompatible Reaction
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGGATATTATTCTACAGGCTCCCCATT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 GACATGACGTGGCTGCATTT?CATCCCATGCTTCAGCTCCTCTTCTACGAATTCCCTTGT 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTICAATTATCICATIGGIGACCATCCGCGTAAIGCTAAGGATTITTATCACTTIGIT 361
                                                                                                                                                                            Contact: Cathy Rouning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GTAGAGTTGGGCCGCCGCCGCAC-TCGGTGGCGGAGCAATCGGTGCCGCTCACATTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGAGTTTCGGTATCTATCCGGGGACTCGGTTTCTTTCACCATCGCAGAATCTAGCGAC
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="p. infestans-challenged leaf"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_nost="50LR"
                                                                                                                                                                                                                                                                                                                                                    /organism "Solanum tuberosum"
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Pred. No. 2.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       /cultivar."Kennebec"
/db_xref="taxon:4113"
/clone="BPL110A14"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156
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162 c
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Best Local Similarity 53.2%;
Matches 293; Conservative
                        (bases 1 to 763)
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                          REFERENCE
                                                AUTHORS
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EST499600 P. infestans-challenged leaf Solanum tuberosum cDNA clone
BPLI10A14 5' sequence, mRNA sequence.
BGS91758.1 GI:13609898
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Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                       /dev_stage="mature green (3.5 days pre-ripening)"
/lab_host="SoLR"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Khol; cLEF - Fruit were tagged at the lcm stage and
harvested 3.5 days prior to ripening. Fruit were cut in
half to verlify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCTCACATTCTTCGACATGACGTGGCTGCATTTTCATCCCATGCTTCAGCTCCTCTTCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 CTCTTACTTATTTTGACCATGTTTGGTTAGGGTTTCGCCGTATGAGGCGGATATTATTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAAAACATTATTCCTCCTCTTAAAAATT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCCGTTAGGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGAATAGCAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 CGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCGTTTATAACGGCTTGGTCTTCAA 540
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                                                                                                                                                                                                                                                                                                                                                                            DB 113; Length 583;
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                                              /clone_lib="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
                                                                                                                                                                                                                                                                                                                                                                       Score 127.8; DB 113; Lengt
Pred. No. 2.3e-22;
0; Mismatches 272; Indels
                                                                                                                                                                                                                                                                                184
/db_xref="taxon:4081"
/clone="cleF3F3"
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al Similarity 51.7%;
291; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Saferidae; euasterida I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 508)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning Generation of ESTs from potato leaves and petioles
Unpublished (2000)
                                                                                                                                                                                                               BG097054 508 bp mRNA EST 29-JAN-2001
EST461573 potato leaves and petioles Solanum tuberosum cDNA clone
CSTB45p9 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482 GGTGATGGAGCTACCATAGTAGGGTTCATTAAGGCGTGGGCTCTACTCCATAAATTCGGT 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 CTGCATTTTCATCCCATGCTTCAGCTCCTCTTCTACGAATTCCCTTGTTCCAAGCAACAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 ITTICAGAATCCATCGTTCCAAAACTCAAACATCTCTCTCTAAAACTCTCATACACTTC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 TTCGTTCAAACCATTATTCCTACTCTTAAACATTCACTCTCCCTCACTCTCAAACACTAC 202
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                 495 AGCGACGCCCCGTCGTTTCTCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACACATT 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Rouning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCGGTTTTGGCTATATGCGTCGGATTTTATTCTACAAGCTACCAATTTCCAAACTCGAT
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Pred. No. 6.9e-20;
0; Mismatches 223; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib-"potato leaves and petioles"
/tissue_type-"leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host-"SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB45P9"
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                                                                                     555 GAAAATGAAGA 565
                                                                                                              GGAGATGAACA 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sateridae; euasterids I; Solanales; Solanaceae; Solanum.

(bases 1 to 564)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning Generation of ESTs from potato leaves and petioles
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST425179 potato leaves and petioles Solanum tuberosum cDNA clone cSTB13B18 5' sequence, mRNA sequence.
                                                                                                                                                                                                                  446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdnafresgen.com.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2000
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                                                                                                                                                                                                                                                 TATCTATCCGGGGACTCGGTTTCTTTCACCATCGCAAATCTAGCGACGACTTCGATGAT
                                                                                                       CTCGTCGGAAATCGTCCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCG
                                                                                                                                                                                                                     CCCATTGTCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTT
                                                                                                                                                                                                                                                                                                                            TTCCCAGGCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACG 501
                                                                                                                                                                                                                                                                                                                                                               DB 142; Length 564;
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/organism="solanum tuberosum"
/cultivar="kennebec"
/cultivar="taxon:4113"
/clone="csrB13B18"
/clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
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Pred. No. 2.2e-18;
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Similarity 52.3%;
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Medicago truncatula
bedrayota; Virdiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida ï; Fabales; Fabaceae; Papillonoidaee; Medicago.
1 (bases 1 to 788)
YandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 ITCCCAGGCCGAGGCGT---CGGTATTGGAATAGCAACGCATCACCGTTAGCGACGCC 503
                                                                  CTGCATTTTCATCCCATGCTTCACCTCCTTCTACGAATTCCCTTGTTCCAAGCAACAT 146
                                                                                                                                                                                                                                            207 ITCCCTCTCTCATGCAATTTÄATCTACCCTTCATCCCGGAGAAAATGCCGGAGTTTCGG 266
                                                                                                                                                                                                                                                                                                                                                                                               TATCTATCCGGGGACTCGGTTTCTTCACCATCGCAGAATCTAGCGACGACTTCGATGAT 326
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EST336180 KVO Medicago truncatula CDNA clone pKV0-1613, mRNA
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Contact: VandenBosch K
                                                                                                                                                       504 CCGTCGTTTCTCGCGTTTATNACGGCTTGGTCTTCAATGAGCAAACACATTGAAAATGAA
                                           CCGCCGCCGGACTCGGTGCCGGAGCAATCGGTGCCGCTCACATTCTTCGACATGACGTGG
                                                                                                                                                                                                                       292 ACACCCTTAGCTGGCAACAT%GCTTGTCCACTAAATTCGAGTGGTTATCCTGAGTTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCATTGTCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTT
  4 ;
  Mismatches 251; Indels
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Tel: 409 845 7707
Fax: 409 845 2891
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Texas A&W University name:T260795e
TIGR sequence name:MTGAU50TK
More information is available at.
http://chrysie.tamu.edu/medicago
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BE187619.1 GI:8666803
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Texas A&M University
  Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

I (bases 1 to 659)

S van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,

Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.

Generations of ESTs from sprouting potato eyes

L Unpublished (2000)

Contect: Cathy Ronning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries

Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WhoI; various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG598154 659 bp mRNA EST 12-APR-2001
EST496832 cSTS Solanum tuberosum cDNA clone cSTS20M23 5' sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                                                                                                                                                     326
                                                                                                                                                                                                   345
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                                                                                                                                                     TATCTATCCGGGGACTCGGTTTCTTTCACCATCGCAGAATCTAGCGACGACTTCGATGAT
                                                                                                                                                                              CTCGTCGGAAATCGTCCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCG
                                                                                                                                                                                                                                                                                                                                                        CAACCTAAGGATGCACCGGGGTCAAACTAGCCGGTCTTAGCCATTCAAGTGACACTT
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                                                                207 TICCCICICICALGCAATITAAICIACCCITCAICCCGGGAGAAAIGCCGGAGTITCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 TCGTTTCTCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 ACCATCGTGAAATTCATAAGAACATGGGGTTTACTCAACAAA 564
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS20M23"
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53.0%;
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163 c
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LOCUS

BG598154

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ACCESSION VERSION KEYWORDS SOURCE

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FEATURES

REFERENCE AUTHORS

BASE COUNT ORIGIN

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Query Match
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                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                            Anote—"Vector: DBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Strategene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
from the red propagated in XLOLR cells."
188 c 100 g 262 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGGTGCCGCTCACATTCTTCGACATGACGTGCCTGCATTTTCATCCCATGCTTCAGCTC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 CICITCTACGAATTCCCTTGTTCCAAGCAACATTTTTCAGAATCCATCGTTCCAAAACTC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 AAACAATCTCTCTAAAACTCTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTAC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCATCGCAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 AATGAATICCACCCTITGGTACCAAAGTIGCAACAA---TCTTITCATITGAAGTAAAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 CTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGTTCCCTTTGTTAGCTATTCAAATAACATCATTCCCAAATTATGGCTTTTCCATTGGC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGTATGATCGAAGTGTGATTATCGACACAAATGACCTTCACGAAGTTTTCTTGAAAGAT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                /tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloli (0 hour)"
/lab_host-"E.coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACAATCTCTTTCTCTCACACTTCCTTTCCTTCCCATTTTC----CGGTACATTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 ACGGTCGCAGAGTCAAATAGCGACTTTGAACACTTGTGCTCCGATTACTCAAGAGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGATAGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 GTTTTCGATAGATCCGTCATAAAATATCCGACGAAATTTGACTCCATTTATTGGAGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 ATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCGTTTATAACGGCTTGG
                                                                                                                                                                                                                                                                                                                                                                                Score 109.8; DB 164; Length 788;
Pred. No. 1.1e-17;
0; Mismatches 292; Indels 6;
Seq primer: SKmod (CTA gAA CTA gtg gAT CC) Location/Qualifiers
                                           /organism-"Medicago truncatula"
/cultivar-"genotype A17"
/db_xref="taxon:3880"
/clone-"pKVV-1613"
                                                                                                                /clone_lib="KV0"
                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                    7.4%;
Similarity 51.1%;
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                                                                                                                                                                                                                                                                                                                    237
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                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
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RESULT

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               EST426515 potato leaves and petioles Solanum tuberosum cDNA clone cSTB21L12 5' sequence, mRNA sequence. BE922746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 TGGTAACCATCCTCGAAAT---GCTAAGGATTTTTATCCCATTCCTCAATTGGCACAACC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 TAAGGATGCACCGGGGGTCAAACTAGTCCCGGTCTTAGCCATTCAAGTGACACTTTTTTC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 GAATCTTGGCATATCCGTTGGTTTTAGTAACCATCATGTCGCTTGTGATGGAAATACCAT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 TTTTCATCCCATGCTTCAGCTCCTCTTCTACGAATTCCCTTGTTCCAAGCAACATTTTTC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 ATCCGGGGACTCGGTTTCTTTCACCATCGCAGAATCTAGCGACGACTTCGATGATCTCGT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGAAATCGTCCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCAT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTT 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 TCTCTCATGCAATTTAATCTACCCTTCATCCCGGGGGAAAATGCCGGGGTTTCGGTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 GACTGGAGATTCTATATCTGTTACTTTTATTGAGACTGATATGAATTTCAATCATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 TGTCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and petioles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.3%; Score 108; DB 142;
52.2%; Pred. No. 3e-17;
live 0; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .574
/organism="Solanum tuberosum"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="cSTB21L12"
/clone_lib="potato leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4113"
mRNA
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                                                                               BE922746.1 GI:10448822
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                                                                                                                                               Solanum tuberosum
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                                                                                                                         potato.
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Matches 290;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tomato.
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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JOURNAL
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BE434257
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S van der Hoeven, R.S., Garvin, D.F., Matern, A.L., Holt, I.E., Liang, F., Van der Hoeven, R.S., Garvin, D.F., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T.S., Ronning, C.M., Craven, M.B., Bowman, C.L., and Tanksley, S.D.
Generation of ESTs from tomato nutrient-deficient roots
L Unpublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescriptSKmcUadapt; Site_1: 5' EcoRI;
Site_2: 3' XhoI; Roots were harvested from plants grown
under the following deficiencies/stresses: 10 mM Al, Zn,
P, K, Fe,N. mRNA was isolated from indivdual treatments.
Proportional aliquots of mRNA of each treatment were mixed
and used for library construction."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liang, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                 BF096979 482 bp mRNA EST 19-OCT-2000 EST400516 tomato nutrient deficient roots Lycopersicon esculentum cDNA clone cLEW18020 5' sequence, mRNA sequence.
512 TCTCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACACATTGAAAATGAAGATGAAGA 571
                                                                                             GACATGACGTGCCTGCATTTTCATCCCATGCTTCAGCTCCTTCTACGAATTCCCTTGT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TGTCAAGTTGCGCCACCTCCCGGCGCGCGACGGAGGTGATACTCCCTCTTACTTTT 63
                     TGAAGAATTTAAAATCTTTGCCAGTTTTCGATAGATCCGTCATAAAATATCCGACGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="tomato nutrient deficient roots"
/tissue_type="roots"
/dev_stage="5-6 weeks old"
/lab_nost="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon esculentum"
/cultivar="TA492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.2%; Score 106.6; DB 144, Best Local Similarity 51.6%; Pred. No. 6.7e-17; Matches 244; Conservative 0; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref-"taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: dfrisch@CLEMSON.EDU.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="cLEW18020
                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                BF096979.1 GI:10902689
                                                                                                                                                  632 TGACTCCATTTATTGG 647
                                                                                                                                                                                    537 AGGGACGATTATATGG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon.
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JOURNAL
COMMENT
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KEYWORDS
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/note-"Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 591)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 24-JUL-2000 EST 24-JUL-2000 EST405335 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG15H6, mRNA sequence.
BE434257 GI:9432100
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Sukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                       CCGGAGTTTCGGTATCTATCCGGGGACTCGGTTCTTTCACCATCGCAGAATCTAGCGAC 314
                                                                                                                                                                                                                                                                                                                                                                                                      304 AATTTCAATTATCTCATTG5TGACCATCCGCGTAAGGCTATTTTTATCACTTG5T 363
                                                                                                                                                                                                                                                                                             244 CCTGAGTTACGTTATGTGACAGGAGATTCTGTGTGTCTGTTACTTTTTTGAGACTGATATG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 CCTAAGTTAGGGGAACCTANGGATGCACCGGGGGTCCAACTAGCCCCGCTCTTAGCCATT 423
CTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTACCCTTCATCCCCGGAGAAATG
                                                                                                                                                                                                                                                                                                                                                                   GACTICGAIGAICICGICGISAAAICGICCAGAAICICCCGITAGGCICTACAACIITGIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 CAGGIGACACITITICCGAMICITIGGIGIATCCATIGGITICACTAACCATCA 476
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/db_xref="taxon:4081"
/clone="clEG15H6"
/clone=llb="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage:"breaker"
/lab_host."SolR"
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Tel: 864 656 4366
Fax: 864 656 4293
Emall: dfrischecLEMSON.EDU
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Contact: David Frisch
Clemson University Genomics Institute
Clemson University
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Search completed: November
Job time: 14896 sec
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1 (bases 1 to 487)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
van der Hoeven, R.S., Bezzeredes, J.L., Ronning, C.M., Nierman, W.,
F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from wild tomato (Lycopersicon hirsutum)
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW616206 487 bp mRNA EST 24-MAR-2000 EST307245 L. hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHT1D15 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                        CCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAA 401
                                 Gaps
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 591;
                               3;
 DB 167; Length
7.2%; Score 106.6; DB 167; Lengt llarity 51.6%; Pred. No. 7e-17; Conservative 0; Mismatches 249; Indels
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Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tax: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prime sequence.
Location/Qualifiers
1. .487
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AW616206.1 GI:7322240
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Contact: David Frisch
               Best Local Similarity
Matches 269; Conserv
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   Query Match
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/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded mixture of cells which is highly enriched for trichome likely with minor contaminations of other types of leaf cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCATTTTCATCCCATGCTTCAGCTCCTCTTCTACGAATTCCCTTGTTCCAAGCAACA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TATGCCCTTAGCCGGAAACGTTGCTTGTCCACTAGATACAAACGGATATCCTGAGTTACG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 104.8; DB 118; Length 487;
Pred. No. 2e-16;
0; Mismatches 232; Indels 0;
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                                                                                                                                                                                                                                                                                                                                    91
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Best Local Similarity 51.3%;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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AB010708 E12753 AB029340 E12756 E12754 AB026494

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Description

SUMMARIES

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FT source 11508 FT /Lissue_type='petal' FT CDS /Crganism='Senecio cruentus' FT /Clone='pCAT48' FT CDS /Product='acyltransferase'. All 1367 Arunes 11508 Arcapanism="unidentified" Ab_xref="taxon:32644" SE COUNT 442 a 293 c 296 g 477 t IGIN Query Match 99.6%; Score 1501.6; DB 10; Length 1508; Matches 1504; Conservative 0; Mismatches 4; Indels 0; Gaps 1 TGAACATTCTGAACATGCCCCCTCGGCACATGGCTCGT 60	241 CTAACACTGATGGTTCGGGTTTTAATAAAAAACCAGAAATAAAACACGTTGAAGGTGATT 300	361 CTCGAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTAT 420 361 CTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCGGAAATGCAATCAAATTAT 420 361 CTCGAAAATGTGAAAACTTTTTATCCTTTCATTGGGAAATGCAATCAAT	ATACAAGGCTCGAAAGTTTTATAAAACTTCCAACATTTAGATGAAATTAAAAGACAACAACAACAACAACAACAACAACAACAACAAC						
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ANDIO708 2 Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
SM Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
SPERMATOPHYTA: Magnoliophyta; Eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Gentianaceae; Gentiana.
SPENJAMA: Tanaka, Y. and Kusumi, T.
Direct Submission
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GDSITLIVASSDQDFPRTHKONSNDLHGLFYWPRISGNLLMPIKSGEMPKFOYSRDE
FPNRGIAVALTAHHFDAKKSPVWFINAMATINFGKNDALLSANLLPSFDRSIIKDL
FRONTETAVALTAHKSKNDDVLEMFSREGKFPRFNKTRATVLSLAGICKLKNKVLNIRGSEPT
IRTTFFTATOGYWTCWKKSDDVVSESSSNDBNELEYFSFTADCRGLLTPPGPPNYF
GNCLAGCWATARELVGDKGLLVANAAIGERIEKRHHNEKOVLADAKTWLSESNGIP
SKRFLGITGSPREDSYGVDFGWGKPAKFDITSVDXAELIXVIGSRBFEKGVELGPS
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                                                  cDNA cloning, gene expression and subcellular localization of anthocyanin 5-aromatic acyltransferase from Gentiana triflora Pplant J. 16 (4), 421-431 (1998)
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/product-*Anthocyanin 5-aromatic acyltransferase*
/protein_id="RAA74428.1"
/db_xref="GI:4185599"
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/clone="pGAT4"
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CGAATCTTCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTATGGCCTAGAGGAAA
                                                                                              GTCCCACTGATAAAGTTCGGTCAACGTTTGTGTTGACCCGAACTAATATCAATTCTACTAA
                                                                                                                                                                                AGAAAAAGGTCTTAA----CCCAAGTGCCAAACTTGGAGTACATGT--CATCTTTACGG
                                                                                                                                                                                              916 AATCATCGAACGACGAGAAATGACCTCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGAC
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                                                                                                                                                                                                                                            988 CCTTAAAAAATGTCGTTTTGACTACGGAAAATGGGTATGCACTTGGTGCTAAAGTAATTG
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                                  595 AAGGATCTCCACCGGTTTTTGATAGATTGATTAACA-----TCCCACATTTAGATGA
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1 (bases 1 to 1703)
Ashikari T., Tanaka Y., Fujiwara,H., Nakao,M., Fukul,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E12753 1703 bp DNA PAT Gentlanatriflora mRNA acyltransferase, complete cds E12753
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JP 1997070290-A/1.
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E12753
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: FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTAT 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 TTCCTAACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAACACGTTGAAGGTG 297
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PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
PI FUKUI YHKO VONDONO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.4%; Score 202.4; DB 10; Length 1703; 52.0%; Pred. No. 1.5e-34;
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 1 18-MAR-1997;
SUNTORY LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/tissue_type='petal
/clone='pGAT4'
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

LOCUS DEFINITION

AB029340 RESULT

9 Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Keiko Sakakibara, Suntoxy Research Center. Fundamental Research, Plant Biotech; Shimamotor-oho, Wakayamadai, 1-1-1, Mishima-gun, Osaka 618-8503, Japan (B-mail:Keiko_Sakakibara@suntory.co.jp, Tel:+81-75-962-8807, Fax:+81-75-962-8262) Fukui, Y., 181 241 304 125 TGACTTTCCACATTCTAAAT:CCATTTCATGGACACTATTGTTCCCAGGCTAAAACAATC 184 364 287 TrcTrrcaccarcaGaarcraggactragactrcGargarcrcgaagaarcgrcaga 346 65 TCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTTCTTCTA 124 62 GCTCACATTCTTCGACATGACGTGCTGCATTTTCATCCCATGCTTCAGCTCCTCTTCTA 121 347 ATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGA 406 TIGGGICACGGICCCACTITITICACTICAAGIGACGITITITICCGGGCTCGGGTATAIC 484 Gaps 64 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla. 185 TTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCTAA 5 CATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGGCCATCGCTTATC 245 CACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAAACAGGTGAAGGTGATTCTGT 2 CGTGATCGAAACGTGTAGAGTTGGGCCGCCGGGACTCGGTGGCGGGGAATCGGTGCC 242 CCCGG------AGBAAATGCCGGAGTTTCGGTATCTATCCGGGACTCGGT 305 TGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACGAAATCATCCTCG AAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGTGA 1 (sites)
Sakakibara, Lamiales; Lamiaceae; Perilla.
Sakakibara, Y., Panaka, Y., Mizutani, M.F., Fujiwara, H., I Ashikari, T., Yamayuchi, M. and Kusumi, T.
Molecular and blochemical characterization of a novel hydroxycinnamoyl-toa: anthocyanin 3-0-glucoside-6 Unpublished (1999) 33; Indels /product="anthocyanin acyltransferase" /protein_id="BAA93475.1" /db_xref="G1:7415646" 12.5%; Score 189.2; DB 12; 48.5%; Pred. No. 1.2e-31; Live 0; Mismatches 738;

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1019 TGGGTATGCACTTGGTGCTAAAGTAATTGGAGAGTCTATATGCAAAATGATATATAATAA 1078
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                          ACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGAA
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                                                                               AGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGAAAGG---ATC
                                                                                                                                   TCCACCGGTTTTTGATAGAT - - - TGATTAACATCCCACATTTAGATGAAAATAAGTTGAG
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24-JUN-1998
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                                                                                                                                                                                                                                                               PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                         Ashikari, T., Tanaka, Y., Fujiwara, H., Nakao, M., Fukui, Y., Yonekura, K., Mizutani, M. and Kusumi, T.
EDED CODING PROTEIN HAVING ACYL, GROUP TRANSFER ACTIVITY Patent: JP 1997070290-A 4 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1479;
E12756 1479 bp DNA PAT 24-J
Perilla ocimoides mRNA for acyltransferase, partial cds
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Location/Qualifiers
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Pred. No. 6.7e-31;
0; Mismatches 657; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism='Perilla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411
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/organism="unidentified"
/db_xref="taxon:32644"
1 316 c 331 g 41.
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                                                                                                                                                                                                                                                                                                                                                                          (C12N9/10,C12R1:19);
strandedness: Double;
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                                                                                                                                                                                                                     Perilla ocimoides
JP 1997070290-A/4
18-MAR-1997
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                     425 TTGCGTCACGGTCCCACTTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTATATC
                                   ACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGGTTCAACTTTTTGAA
                                                                                                                AGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGAAAGG---ATC
                                                                                                                                    527 GGCTTGGTCTTCAATGAGCAAACACATTGAAAATGAAGATGAAGATGAAGATTTAAATC
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24-JUN-1998

E12754 1622 bp DNA PAT 24-JU Gentlanatriflora mRNA for acyltransferase,complete cds. E12754 E12754 GI:3251586

DEFINITION ACCESSION VERSION

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ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 TCAAAGTTCTTGAGAAATGC3GTGTTGCGCCACCACCGGACGCCGTCGCGGATTACAG
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0; Mismatches 643; Indels
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/clone='pGAT106'
35. .1474
/product='acyltransferase'
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Ashikarl,T., Tanaka,Y., Fujiwara,H., Nakao,M.,
Yonekura,K., Mizutani,M. and Kusumi,T..
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER
SUNTORY LID
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/organism="unidentified"
/db_xref="taxon:32644"
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JP 1997070290-A/2
18-MAR-1997
30-JAN-1996 JP 1996046534
17-FEB-1995 JP 95P 67159
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strandedness: Double;
topology: Linear;
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JP 1997070290-A/2.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Gentianaceae; Gentiana.

acyltransferase homolog. Gentiana triflora cDNA to mRNA. Gentiana triflora

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

L (slues)
Yonekura sakakibara,K., Tanaka,Y., Fukuchi-Mizutani,M.,
Yonekura sakakibara,K., Toshihiko,A., Yamaguchi,M. and Kusumi,T.
Wolecular cloning and biochemical characteization of
hydroxycinimamoyl-Coa.anthocyanin

AUTHORS

TITLE

REFERENCE

3-0-glucoside-6-0-hydroxycinnamoyltransferase from Perilla frutescens and diverse plant acyltransferase homologs

Unpublished (1999) 2 (bases 1 to 1622) Tanaka,Y. and Yonekura-Sakakibara,K.

JOURNAL REFERENCE

AUTHORS

Direct Submission

TITLE JOURNAL

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CGGGGGAGGAATTACCACTTTTGCTTTACAGGTGACGGTGTCTCCCAACACGGGTA
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Submitted (21-APR-1999) to the DDBJ/EMBL/GenBank databases.
Yoshikazu Tanaka, Suntory Ltd., Institute for Fundamental Research;
Makayama-dai 1-11, Shimamoto, Osaka 618-8503, Japan
(E-mail:Yoshikazu Tanaka@suntory.co.jp, Tel:81-75-962-8807,
Fax:81-75-962-8262)

Location/Qualifiers

source

FEATURES

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HLHFYRERHDCPNSKFITSSTKSSLSLVLKHFLPLAGNLIWPDSSDRWPELFRKGD
SVSLTIAESSMDFDYLAGDHQRDSYRFNDLIPQLPEDTVJCSDEVLEFALQVTYSN
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GISLPKNRMDAFAITFINFINSLHRSPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                     /translation="MAGNSEDIKVLEKCRVAPPPDAVAEFTVPLSFFDMRWLISDAEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.2%; Score 138.2; DB 12; Length 1622; 48.6%; Pred. No. 2e-20;
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                                                                                                                                               homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 643;
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35. .1474
                                                                                                                                             /product="acyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                 б
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                                                                                                                             /codon_start=1
                                                                                                    /gene="GAT106"
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AB026494 1622 bp mRNA PLN 04-APR-2000 Gentiana triflora GAT106 mRNA for acyltransferase homolog, complete ods.

AB026494 LOCUS DEFINITION

RESULT

us-08-894-356c-5.rge

	RESULT 8 AC002560 LOCUS AC002560 101176 bp DNA PLN 19-JUL-2000 LOCUS DEFINITION Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome I, complete sequence. ACCESSION AC002560 VERSION AC002560.2 GI:92:1167 KFWANDROS HTG	χ a s	Shinn, P., Altafi, H., Bel, Q., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Theologis, A. and Ecker, J.R.		AUTHORS ECKET, J.R. AUTHOR JOENNAL Submitted (13-NOV-1997) Arabidopsis thallana Genome Center, JOENNAL Submitted (13-NOV-1997) Arabidopsis thallana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA REFERENCE 4 (bases 1 to 101176) AUTHORS ECKET, J.R.	Direct Submission Submitted (26-JAN-1998) Arabidopsis thaliana Genome Cen Bepartment of Biology, University of Pennsylvania, 38th Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, 0 (bases 1 to 101176) Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, O.,	Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vayaberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. TITLE Direct Submission Journal Submitted (28-JUN-2000) Arabidopsis thallang Genome Center,	Department of Blology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA REFERENCE 6 (bases 1 to 101176) AUTHORS Ecker, J.R. TITLE Direct Submission JOURNAL Submitted (15-JUL-3000) Arabidopsis thaliana Genome Center, Hamilton Walk, Philadelphia, Dennsylvania, 38th Street and	REFERENCE 7 (bases 1 to 101176) AUTHORS Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, O., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howling, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Tortuni, M., Vaysberg, M., Vu, G., Davis, R., Federspiel, N., Theologis, A., and Ecker, J.	Infect Submission
Qy 301 CTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATATTTGACAGAAATCATC 360	0y 361 CTCGAAAATGTGAAAACTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTAT 420	Oy 481 TATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCGGTTCAACTTT 540 b 111 111 111 1111 1111 1111 1111 1111 1111 1111 1111 111 11	583 CTTTTTAACCAAAGGATCTCCACCGGTTTTTGATAGATTGATT	Oy 703 GTCCCACTGATAAAGTTCGGCTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAA 762 Db 762 TTTCTAAAGATGAGGTCGAGCCCTTCATCCTACCCCTATTGATATCATGAAGCTCA 821 Oy 763 AGAAAAGGTCTTAACCCAAGTGCCAAACTTGGAGTACATGTCAT 807 Oy 763 AGAAAAGGTCTTAACCCAAGTGCCAAACTTGGAGTACATGTCAT 807 Db 822 AGAAATCATTTCGTCAAAAAATCGCAACTTAACCGGTAGTAATATAATCTGTCAA 881	808 882 868	942 TAAGAGAGAGGGATAAACATGCAGCAACTTATGTGCTTTCATCAACTGCC 922 GATCTCGTCTTGATCCACCAATTCCCACACCTACTTTGGTAACTGTGGGCCCATGTG	982 TCCCGACCTTAAAAANTGTCGTTTTGACTACGGAAANTGGGTATGCACTTGGTGTTGATGTTAAG 1062 TGGTGGGATCGACTCATGAGCAACTTGTAGGAATGAGGTTTCTCGGTACTTGATGAGGTTTTCGATAGGTTGTAGGAACTGTTGTAGGAACTGTTGTAGGAACTGTATATGAAGGTTGAAGGTTGTAGAAGGTTGTAAGGAGTTGTAAATAAT	0y 1102 CGAGATGGCATGTTCATGATCCGG	Oy 1207 AGTATGAGACTGTTTCAATAGACTATAATACGTCGATTTCTATAAATGCAAGAA 1263 1 1 1 1 1 1 1 1 1 1	Oy 1324 CTAGCATCTTT 1334

CDS

FEATURES COMMENT

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.12303,12448. .12519,12596. .12685,
                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mrgFSSvSswLwTsvEIGEVFLGSTTWLDAVAvAEDAVDwwvFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAEVVSLFFDDCSKLINTMSISLERPDNVDFKQVDSGVHQLKGSSSSLCFVLSVGARR
VKNVCISFKECCDVQNREGYSSNSHTNCDNDIWHRCLRCLQQVDYEYKMLKTKLQDLF
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ISSSTGSLBELSNLILCHHUTGSIPPELSQYTLRIDLKRNSTGSISBASLPPSLQY
LSLAWNQLTGSVYTHLIRLNQLNYLDISLNRFTGTIPARVFAPPITHLQLQRNFFFGI
IQPANQVTISTVDLSYNRFSGGISPLLSSVENLYLNSNRFTGEVPASFVBRLLSANIQ
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GGETPSPYCHYMDIAAQKWLVIFSGNNGNBILIDDTWALDTROFFSWANDPS
GRWYSSGSREDGIFLLCGGIDHSQYTLGDTYGLKMDSDNVWTPVPAYAPSPRYQHTA
VFGGSRLHVIGGILNRARLIDGEAVVADTNQPETSASGANRQNOYQLMRRCHHAAASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AWKCVVVLRGWGLDQIGWRSVGNWVFSVRFVAGPASSLVRDLRQDSYTSANDLVPVVV
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SKFFESWDFTSDPCGFAGVYCNGDKVISLNLGDPRAGSPGLSGRIDPAIGKLSALTEL
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19064..19139,19214..19410,14947..15955,19668..19752,
19865..20103,20179..20253,20345..20649,20798..20902,
21088..21216,21356..21437,21513..21608,21780..21849,
21929..222025,22408..22552,22586..22659,22810..22888,
23041..23101,22206..23315,23411..23555))
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         SVAIVFSTEMRAYSRVYGPIKDLLSAENPAKYRDCTLTEFSTIFSSKTLDAPKLHHFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16495. .17682
//note="similar to protein kinase pir||A57676; similar t
ESTs gp|A199361.1, dbj|AV538995.1, dbj|AV522524.1, and
dbj|AV538995.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 37271 AACATCGAGACCTGTCACATCTCTCCCCCAAAGGGCACCGTTGCATCCACCACTTT 37330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 101176;
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Pred. No. 3.5e-15;
0; Mismatches 698; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(11965. .12033,12173. .12303,12448.
12756. .12915.12985. .13041)
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                                                                                                                                                 similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVSFKLCENLLVLLLEKQILQAGGTIPQVDIN"
                                                                                                                                                                                                                                     /evidence=not_experimental
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Best Local Simil
Matches 613; C
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                                                                                                  CDS
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SQAKAFDETKTGYKGLVASGIKEIPAMFHTPPDTLTSLKQTAPPSQQLTIPTVDLKGG
SQAKAFDETKTGYKGLVASGIKEIPAMFHTPPDTLTSLKQTAPPSQQLTIPTVDLKGG
SMDLISTRSVVEXTGDAATGRFQVVNGIGSVEVMERMKEGIRRFHEQDEFKKREY
SRDHTRDVLYYSNIDLHTCKRAANRRDTLACYMAPDPFKLQDLPAVGGEIMMEYSKQL
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ITTLLQDNYGGQVYTHQCWPDVSPYPGALVINIGDLACISNSKFISREHRVIANGS
SEPRISMCFYSTFMKPNRYYPTKELLSEQNPAKYRDLTTEFSNTFRSQTIRITE
IPALFRATPATLASLKSPPPRHLTIPTVDLKGASVVEKIGEAAEKWGLFHLVNNGIP
VEVLERMIGGIRGFHEQPEPRHKTTTPTVDLKGASVVERIGEAAEKWGLFHLVNNGIP
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VGVLERMIGGIRGFHEQPEPRHKTTTTVLLGONVGLCOYFHERDYDACARSOYN
VQHYPPCPOPDLTIGINHEYDISFLTVLLLONNGHLCARSOYN
VQHYPPCPOPDLTIGINHEYDISFLTVLLQDNVGGLCOYFHSDENTINNINT
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KVEPIQWWDVCRRSDWLETEERLPKSTTEKQYDLETVSNHLTSHEDACLSLDMNSHFS
ELEXYLKSCSERPPERSHCYLSNFEVKYTSGMLEVWQNSKISHTWBDSPRDSSSTGGEF
ELEXYPAHELEIKQKKLLPVPDHFHSYRATLEDRFSMCYHSATGSHQVNGKICQDI
INCHSKPGSLESAESSEEGSTRQMENHDSDHMSNSIKSSLPLYPTWGIYKETEKNN
ANGWMEKPVTAKLSTLKETRITNGFTTPPILLTDSVNEQMLSTGKPPMGFGFALHEEHC
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CFSQQSQWVAIISSKGTCHIFVLNSSGSDAAFQPCEGEEPTRLPASSLPWWFTQSLSS
NQQSLSPPTAVALSVVSRIKYSSFGWLNTVSNATTAATGKVFVPSGAVAAVFHKSVTH
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NLDDIIGARVFTPSVYFYPSTNNRESFVLKRLQDALSEVLVPYYPLPSGRLREVENGKL
EVFFGEEGGVLMVSANSSMDLADLGDLTVPNPAWLPLIFRNPGEEAYKILEMPLLIAQ
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PPMVKYPHHEYLPIEERSNLTNSLWDTKPLQKCYRISKEFQCRVKSIAQGEDPTLVCS
TFDAMAAHIWRSWVKALDVKPLDYNLRLTFSVNVRTRLETLKLRKGFYGNVVCLACAM
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FEMYETADFGWGKPVYAGPIDLRPTPQVCVLLPQGGVESGNDQSMVVCLCLPPTAVHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(736. 1038,1276. 1713,1874. 2119,2205. 3032, 3117. 3274,3483. 3610,3725. 4134,4313. 4435) //note="unknown protein: similar to ESTS dbj|AV529515.1, dbj|AV529266.1, dbj|AV54950.1, dbj|AV523761.1, dbj|AV523761.1, and dbj|AV543761.1,
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//note="unknown protein; similar to ESTs gb|T04168.1,9p|T21964.1, and gb|AW004462.1"
Submitted (19-JUL-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On Jul 15, 2000 this sequence version replaced g1:2618677. Location/Qualifiers
                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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/note="hypothetical protein"
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/product="F21B7.1"
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/db_xref="G1:9280672"
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/db_xref="GI:9280671"
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123 TATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAA
                                       TTCTCTTACCAAAACTCAACTGAATCTTTCCTCCAAGACTTTGTACCCAACCTCAAACAT
                                                                                                     GTTGTGCTTACTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATCCT
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                                                                                                                                                                                                       37511 GGTCCCGACCCTCCATATTTACACTACAACGCTG---GCGAAGACTCTCTTGTTTTCACC
                                                                                                                                                                                                                                                                                                                                                                       GATTGCGTCACGGTCCCACTTTTTTCACTTCAAGTGACGTTTTTTTCCGGGCTCGGGTATA
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                                                                              TCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCT
                                                                                                                                                                AACACTGATGGTTCGGGTTTTAATAAAAACCCAGAAATAAAAACACGTTGAAGGTGATTCT
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Busaryotta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 119914)
Federspial, N. A., Palm, C. J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskala, I., Klm, C., Lenz, C., Li, J., Liu, S., Walker, M., Yu, G., Schwartz, J., Shinn, P., Toriumi, M., Vysotskala, V.S., Unpublished
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Genes with similarity to proteins in the databases are described
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FederSpiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Bcker, J., Theologis, A. and Davis, R.W. Submission

Submitted (30-JAN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 119914)
Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R. Au, M., Araujo, R., Buchler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V. Vi, G., Ecker, J., Theologis, A. and Davis, R.W.
Direct Submission
                                                                                                                           38522 ATCGCATTCTCAGAGTCCAGAGACGGCAGCAATGGAGTTGAGATTGGAATAGCACTAGAG 38581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremehetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Lucos, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskala, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Dec 30, 1998 this sequence version replaced gi:2734094.
Bases 1-9262 of clone F21M11 overlap with bases 6899877825 of
"TAMU' BAC clone F20D22 (ACO0241) and bases 119525-119914 of
F21M11 overlap with bases 1-389 of "TAMU' BAC clone F21B7
                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-1999
genomic sequence,
GATTTTGGATTAGGAAAGCCCTGCAAAATGGAGATAGTGCACATAGAAACAGGTGGTTCT
                                                               ATTTCTATAAATGCAAGCAAACATCAGCACAAGATCTTGAAATTGGATTGAGTCTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                     PLN
I BAC F21M11
                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                             38582 AAGAAGAAATGGATGTTT 38602
                                                                                                                                                                                           1302 AGTATGCAAATGGAGGCGTTT 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA 94304, USA
3 (bases 1 to 119914)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC003027.1 GI:4079614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thale cress.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                     119914 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     AC003027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                               1242
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JOURNAL
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JOURNAL
   38462
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
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AC003027
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join(20752. .20994,21362. .21497,21596. .21740,21825. .21994,
22102. .22178,22542. .22758,22920. .23064,23343. .23442,
23599. .23693,24021. .24072,24227. .24298,24441. .24647)
/gene="F21M11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /COGOD_STATE_1
//COGOD_STATE_1
//COGOD_STATE_1
//DOCUSTO.STATE_1
/
                                        DSLHNPTKEVYTQDIGDKTEEIDSKLRRSNETVRDGNHYDGGGVLNPVENLTOWKSAK
SKGRTKOKOGSQKENSNFIADQEEKRDSSSFGTDBQIDDITLSVWFKOR TE BFKLINQE
LAVDASCHGWLSTESGSGENSASMYTLTPEKLKSTSCYSKPLRINDDBPVLCALTL
EDIKQFSATSTPRKSPSKSPDETPIIGTVGGYWGNRSKAIDCGSASSFKGIPNTSSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IINAAWMKASLKASQPVDEEPFEIQIDTQGCQDGPKTARLRAETNKPKLFEGLKFYFF
GDFYKGYKEDLQNLVKVAGGTILNTEDELGAESSNNVNDQRSSSIVVXNIDPPHGCAL
GEVTIIWQRANDAEALASQTGSRLVGHTWVLESIAGYKLHPVIG"
20752. 24647
/gene="F21M11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MNTKTMRLPPRRVLTADKRKERDAFISSVTDNPPEIAKFPSPPP KLVPPPVNPISKKSSTAAAEPIGSNQLMLAGYLSHEYLTGGTLFGEGWNQARAQAESS KIKPSHTVEPAEECEPKRKRYREVANLLRSDGAQLPGIVNPAQLARFLKL" complement (29264. . . 32033)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WDYEDFLLLCPAHSSVKFPNEKSGHRVSRAEPLPKINPAELCSLEQTPAFTKELVLCG
SALSKSDKKLMESLAVRFNATISRYWNPSVTHVIASTDEKGACTRTLKVLMGILNGKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGTLFKAIEDYDPDSKRMLHQLKKYVPFFVIRNĪAHRSSLAGFLLYHDDPVFNPLTPW
PRPPTKNVGCIYGAHLKTPSVGYYFABSGRPYPDMNITDIJTSTBGSLVSRSGTVVDG
NACPITGDETVPYHSLSWCKNWLGPRVNITMAPQILIGKIKQDPEHDGSDVHVELNVD
HEHGSDIIANMTKAPRVKYITFYEDSESIPGKRTAVWELDKSGY
        TDDQIIEVASNSSGSYPENHRYKNCRESDDDIEEDEFDCSDSDLDEDEEYYSDVGFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(29264. .31015,31312. .31414,31484. .31587,
31782. .32033))
                                                                                                                                                                                                                                                                                                     complement(join(16835. 17185,17274. 17392,17491. 17656
17795. 17885,17982. 18079,18175. 18361,18504. 18604,
18705. 19049,19134. 19349,19439. 19791,19862. 19967,
20188. 20238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Unknown protein; Location of ESTs 203124T7, gb|H76794 and 203124XP, gb|AA605510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 119914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 1.9e-09;
); Mismatches 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Hypothetical protein"
                                                                                                                                                                                               REDKSVNWHSTPFEARLEKALNNIDK"
complement(16835. .20238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAD10670.1"
/db_xref="GI:4204289"
                                                                                                                                                                                                                                                                             /gene="F21M11.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27777. .28734
/gene="F21M11.6"
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28007. .28465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F21M11.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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Best Local Simi
Matches 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRRNGERGLAMTVYNNASPSSSRLSMEPEEVPPMYLLPAHPMETKVSEASALVILND
EPNIDHKPVISDTGNCSAPMLEMGKSNIHVQEWDWETKDILNDTTAMDVSPSSAIGES
SEHKVAAASVELASSTSGEAKICLSFAPATGETTNLHLPSMEDLRRAMEEKCLKSYKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHPEFSVLGFMKDMCSCYIDLAKNSTSQLLETETVCDMSKAGDESGAVGISMPLVVVP
ECETSGDGMSKAISNNKDITAGEBNVETPWNBIETNEKYPSFRYMPHSFYFQDAPVIFS
LSSFSDBGGSCSTAISNEDTAGEBNVGNETPWNBIETNEVPSFRYMPHSFSFSARDO
RSFSDBGGSCSTSGIBGLASEMSCNCAIGVDNGFAYTLDGLLKEFFLEARISEARDO
RKQVLRFCEECPLERAKKVEILEPCKGHLKRCAIKECWFKGGCTKRCNRVVQRGMHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /proteIn_id="AaD10667.1"
| DackeIn_id="G1:4204286"
| /translation="kLDQ158HTHEKLSVETAEPHHLNDRVHIVEEIPKASVIPITE
| ICDEAEEKCSPSTISRKRVTFDSKVKTYEHVVSEESVELSEEKNEEVESEKRSLKSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Proteins in this region are annotated in the F21M11 entry, AC002411." 1.\ 9262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="WAPDLETKRACDAMKILGISETKTRAFIRKILKTYENNWDFIEE
DAYKVLLDAIFDEADAQSTEKNKKEEEKKKREEKKSRSVATSRGRRAAPEPLVQDEE
DDMDEDEFPLKRRLRSRRGRASSSSSSSSYNNEDLKTQPEEEDEDDGVTELPPLKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLQVFFTPNGKGWGLRTLEKLPKGAFICEYIGEILTIPELYQRSFEDKPTLPVILDAH
WGSEERLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDRTMFLSLTIASLLVGVVSAGDWNILNQLRGLGSSSSQNGIVS
KGIKTDLKGYCESWRINVEVHNIRKFDVVPQECVSHIKDYMTSSQYKDDVARTVDEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHFGSMCCSKSKCDGMDAWIFDIDDTLLSTIPYHKKNGFFGGEKLNSTKFEDWIQKKK
APAVPHWKKLYHDIRERGIKIFLISSRKEYLRSATVDNLIQAGYYGWSNLMLRGLEDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKEVKQYKSEKRKWLMSLGYRVWGVMGDQWSSFAGCPLPRRTFKLPNSIYYVA"
complement(join(14004. .14312,14565. .14641,14787. .15831,
15906. .16006,16327. .16362))
(Informatics Group, Oak Ridge National Laboratory, http://compblo.cnnl.gov/section/index.html, GENSGAN (Chris Burge, http://gnomblo.cnnl.gov/section/index.html), GENSGAN (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
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complement(join(14567. .14641,14787. .15831,15906. .16006,
16327. .16362.)
/gene="F2IM11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="overlap with bases 68998-78259 of 'IGF' BAC clone F21M11."
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join(13033. .13488,13717. .13926,14139. .14514)
/gene="F2LM11.2"
/gene="F2LM11.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Unknown protein; Location of ESTs 40C3TT, gb|AA728590 and40C3T7, gb|T04573"
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/gene="F21M11.2"
                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Hypothetical protein"
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complement(14004. .16362)
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/db_xref="G1:4204284"
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/db_xref="GI:4204285"
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/gene="F21M11.1"
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46073 TTCTCTTACCAAAACTCAACTGAATCTTTCCTCCAAGACTTTGTACCCAACCTCAAACAT 46132
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AACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGGCCATCGCTCGTTA
                                                             TCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTTCTTC
                                                                                                                                                                                        TCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCT
                                                                                                                                                                                                                                                                                   46193 CGTCCCGACCTCCATATTTACACTACAA - - - CGATGGCCAAGACTCTTTTTTCACC
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/TEACH 101 - MAAIENRVTLKKHEVTKVTPFVNPNSKTTSFTLDLTYEDFFWFK
WEDPVERLEFFERDLTWDLTABLDAAKHENDAAKPAVY
YEPDONDGYSFAVARSSECHAGFHILSGNGIRGAVEFHPLVPQLSJTDDKABVIA
TILFPNGGFSIGVSSHHAILDGKTSTLFLKSWAYLCKQLQLCHHPCLSPELTPLLDRT
TYLFPNGGFSIGVSSHHAILDGKTSTLFLKSWAYLCKQLQLCHHPCLSPELTPLLDRT
KLERKYNHOLSKSSKGVBLSSTFVLTAVPVCWAKAKLAKAKTEREATEDIT
KLERKYNHOLSKSSKGVQRLSTFVLTAVPVCWAKAKLAKAKTEREAAGNBEIKN
IIVGFTADYFSRLDPPIPLNYFGNCNGRHCETAKASDFVGNGVAKVAKILAKAKTEREAAGNBEIKN
ANSLAERRDGGGGVVLEKGAMIFSVAGSPFOVGSBFGWGRPKKVEIVSIDRTQ
ANSLAERRDGGGGVVLEKGOMIFSVAGSPFOVGSBFGWGRPKKVEIVSIDRTQ
344 C
354 G
46 E
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Fruit flavour related genes and use thereof
Patent: WO 0032789-A 40 08-JUN-2000;

AHARONI ASAPH (IL); VERHOEVEN HARRIE ADRIANUS (NL); LUECKER JOOST
(NL); CPRO DLO (NL); CONNELL ANN PATRICIA 0 (NL); TUNEN ARJEN
JOHANNES VAN (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 1648)
Aharoni, A., Verhoeven, H.A., Luecker, J., O'Connell, A.P. and Van
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                                                                  47204 ACAGGTGGTTCTATCGCATTCTCAGAGTCCAGAGACGGCAGCAATGGAGTTGAGATTGGA
                                                                                                                                                                                                                                                                                                1290 TTGAGTCTACCGAGTATGCAMATGGAGGCGTTTTCTAGCATCTTTGATGAAGGATTAGAG
                                         GAACCTTTCATGATCCCGGCTAGGAAG---ATTGGTGTTGCTGGTACACCTAAGCTCAAC
                                                                                                                           1170 TTGTACGACTTTGATTTTGGGTGGGGGAAGCGCATAAAGTATGAGACTGTTTCAATAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT
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WO0032789
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/db_xref="GI:10187185"
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/organism="Citrus limon"
/db_xref='taxon:2708"
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/codon_start=1
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For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgl-bin/add_graph.cgl/c=MXFI2
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
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Skaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asamizu, E., Sato, S., Kaneko, T., Nakamura, Y., Kotani, H., Miyajima, N.
                                                                                                                                                                                                                                                                                          1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structural analysis of Arabidopsis thaliana chromosome 5. VIII. Sequence features of the regions of 1,081,958 bp covered by seventeen physically assigned Pl and TAC clones DNA Res. 5 (6), 379-391 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
                                                                                                                                                                                                                                  1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1421
                                                                                                                                                                                                                                                                                                                                            GGTTGCTTTTGTTGCAGAGATGTTAAGTGATATGGTCAAAGGGATCGATGCGGATGCCAT 1241
                                                                                                                                                                                                                                                                                                                                                                                                 1079 GGACGGAATCTTGAAAGATGCCGCGAGATGGCATGAACCTTTCATGATCCCGGCTAGGAA 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGCATAAAGTATGAGACTGTTTCAATAGACTATAATACGTCGATTTCTATAAATGCAAG 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAACATCAGCACAAGATCTTGAAATTGGATTGAGTCTACCGAGTATGCAAATGGAGGC 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1242 TGAAGCCAATGATGATAAGGTTTCAGAAATATTGGAAATTCTGAAAGAAGGAGCAATGAT 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1002 CAAAGCCAAAACTGAAGCTGAAGCTGCAGCAAATAATGATGAAATTAAAAATATTATTGT 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB016892 66237 bp DNA PLN 27-DEC-2000
Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MXF12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (18-AUG-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research: 1532-3, Yana,
Kisarazu, Chiba 292-0912, Japan (B-mall:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                               1062 GGGATTCACTGCGGATTATAGGAGCCGTTTGGATCCTCCAATTCCACTTAATTTTGG
                                                                                                                                                                                                                                                                                       1022 GTATGCACTTGGTGCTAAAGTAATTGGAGA----GTCTATATGCAAAATGATATAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1122 TAACTGCAATGGGAGACATTGTGAGACTGCAAAAGCAAGTGATTTCGTTCAAGAAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1422 AAGAGATGGAGGCGGCGTTGAGGTTGGAGTTGTTTAGAGAAGCAACAAATGGAGGT
                                                       902 CATAATCACCATTGATTGTCGATCTCGTCTTGATCCACCAATTCCCACAGCCTACTTTGG
                                                                                                                                                                       962 TAACTGTGGTGCACCATGTGTCCCGACCTTAAAAAATGTCGTTTTGACTACGGAAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein similarity are described as "unknown protein".
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compble.ornl.gov/Grail-1.3/),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTTTCTAGCATCTTTGATGAAGGATTAGAGAGTCAAGTTTCATTGTAGATCAT 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB016892.1 GI:3449333
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TITLE
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PDDVYATSRSMGNADHPEQNLNFNLTWLFTVDAGFSYLVRLHFCETLSEVNKEGQRVF
SIFIENQTATLEMDVFRMSGGSWIPMYLDYTVIAGSGSGRRHDLRLDLHPLVSINPKY
YDALLNGVBELKMNPPDGRAGGSWIPMYLDYTVIAGSGSGRRHDLRITALNTLAVYS
SLVALLNGVELLKMNPPGRALAGPNPDPLVSPDLIPMRATPRRKNKSHLPITLAVYG
SLVALAMFVVGVLVIMKKKSKPSTNSSWCPLPHGTDSTNTRPAKSLPADLCRFTE
FEIRSATINPFEDKLIIGVGGFGSYVKGQIDGGATLVAVKRLETTSNOGAKEFFTELEM
LSKLRHVHLVSLIGYCDEDNEMVLVYEYMPHGTLKNDHTSDPPLSWKRRLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVKGTFGYLDPEYYRRQVLTEKSDVYSFGVVLLEVLCCRPIRMGSVPPEGADLIRWVK
SNYRRGTVDQIIDSDLSADITSTSLEKFCEIAVRCVQDRGMERPPMNDVVWALEFALQ
LHETAKKKNDNVESLDLMPSGEVGTTTDGEDDLFSRTTGHVGKSTTTDDSVLVVGDER
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KMAKKETDVIRLSGGPRIPMYLDFSVYVGFESGMIQPELRLDLVPLKDTWQTYYDAIL
SGVEILKLNDSDGNLARPNPELLVSTDSTPDDSNVTPPIKGKPHVLVIILIVVGSVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVYRGNLSNGRTVAVKVLKDLKGNGDDFINEVTSMSQTSHVNIVSLLGFCYEGSKRAI
ISEFLEHGSLDQFISRNKSLTPNVTTLYGIALGIARGLEYLHYGCKTRIVHFDIKPQN
ILLDDNFCPKVADFGLAKLCEKRESILSLIDTRGTIGYIAPEVVSRMYGGISHKSDVY
                                                                                                                                                                                                                                                                                            It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MIRHALLIFSILVSTPIVGEGATSTYEPTDVFLENCGDTSNNVD
VSGRNWTARDKYLLSSNLVNASFTAGASYQESVOKJPPYMARIFRSEPETYSFPYTPG
VSGRNWTARVPTRYCSORNAVKSFSVKVNGFFLLNNSSADLTVKASKPOTETIKEFI
IPVYQTLNLTFTPSLDSLASFVNGIEIVSIPNRFYSKGGFDDVIINVGSSVDFHIENST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNCNVLFLLSVLVSVTACVTAAYHPTDVFLFNCGDTSNNVDNSG
RNWTVESRQILSSNLVNASFTSEASYQKAGVSRIPYMKARIFRSEFTYSFPVTPGSIF
LRLYFYPTQYKSGFDAVNSFFSVKVNGFTLLRNFNADSTVQASIPLSNSLIKEFIIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HQTLNLTFTPSKNLLAFVNGIEIVSMPDRFYSKGGFDNVLRNVSSDVDFQIDNSTAFE
SVHRLNVGGQIVNEVDDSGMFRRMLSDDSFGNSGSIVNVPGVKINYTEKTPAYVAPYD
                                                                                                                                                                                                  (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is K15E6 and the 3' clone is K3K3.

Location/Qualifiers
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GMSYRDPGTSNRTVVMGRAKIRLSPLMTSYKERPISGGIDLVGLNSDQCVVKKGYLTY
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KMILVSLWCIRPCPSDRPPWNKVVEWIEGSLDALELPPKPSRHISTELVLESSSLSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGAARGLQYLHTGAKYTIIHRDIKTTNILLDENFVTKVSDFGLSRVGPTSASQTHVST
of
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="receptor protein kinase-like protein"
/protein_id="BaB10826.1"
/db_xref="G1:10177547"
                                  Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendedl, Stanford University,
http://grenninn.cool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="receptor-like protein kinase"
/protein_id="BAB10824.1"
/db_xref="G1:10177545"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="gene_id:MXF12.2"
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/note="gene_id:MXF12.3
unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Columbia"
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/evidence=not_experimental
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/db_xref="G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTAACTGTGGTGCACCATGTGTC--CCGACCTTAAAAAATGTCGTTTTGACTACGGAA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1197 AAGGGGATAAAGTATGAGACTGTTTCAATAGACTATAAATAGGTGGATTTCTATAAATGCA 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       899 GTTCATAATCACCATTGATTGTCGATCTCGTCTTGATCCACCAATTCCCACAGCCTACTT 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26478 GTTGCATTGAAGATTCCAGAGATTTTGGAAGGGTTTACGACTCTTTCACCAGGAACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1017 AATGGGTATGCACTTGGTGCTAAAGTAATTGGAGAGTCTATATGCAAAATGATATATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1077 AAGGACGGAATCTTGAAAGATGCCGCGAGATGGCATGAACCTTTCATGATCCCGGCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 66237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72.6; DB 12;
Pred. No. 5.1e-06;
0; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
WO0111061.
              32432. .33823
/note="gene_id:MXF12.10"
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synthetic construct
artificial sequence.
1 (bases 1 to 1141)
Kunst, L. and Clemens, S.
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Sequence 22 from Patent
AXO83744
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                                                                         /codon_start=1
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Matches 22
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VRLINVGRMADDPYLMFRRMLSDDYEFLIGGVSPYMPDNVISYTERTPAVYAPAY
VYSTCRMAGNAQDTYLNLNFNLTWLFTYDAGFSYLVRLHFPERYLNRANGRVFSIELG
NOMAREEMDVIRLSGGPRIPIYLDFRIYVGSESGPRPDLRLDLHPLVKDNPFYFRAIL
NGYEILKLINNSGNLAILONDELKPUPPSNUTPNHYTQVIRGKSSHLLVKIFFAVGP
GTGLAFFVVVLLMLMRQMKRRNKRERVVMFKLLLNNYTYAELKTTRSSYTIGKGG
FGTVYGGNLSNGRKVAVKLKDLKGSAEDFINEVASMSQTSHVNIVSLLGFCFEGSKR
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LEHGYVEAAANGFGRYFALICOYSSIAVSOAK PDAGKIVIGTIALIGSTTNILLYPKF
GRIIDIVSRDVATPEQGTSLIAVRAVIIILLIVVIGSICTALRAMLFNSASERVV
ARLRKDLFRHLANGETAFYDVTKTGELLSRLEDTQIIKNAATTNILSBALRNYTALI
GVGFWFTSSWKLTLLALVVVPVISVAVKQFGRYLRELSHTTQAAAAVAASIAEESFGA
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TITTYGSMYVGALTSFILZSYSSYSSLSSLYTAMKAAGARRRVGDLDRYSSMS
SSGDKCPVGAPDGDPELNDVWFAYFSRPSHMTLKGISLRLTPGSKVALVGPSGGGKTT
IANLIERFYDPLKGKILLLNGVSLMEISHQYLHKQISIVSQEPILFNCSVEENIAYGFD
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VLLLDEATSALDAESEYLVQDAMDSLMAGRTVLVIAHRLSTVKTADCVAVISDGEVAE
KGTHDELLSLNGIYTNLVKRQLQSSSSVTTL"
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AVERVIFKTATDASRPFEDSVIVPNLKTSLSSSLSHYLD-LAGKLVWEPLDPRPKIVYT
PNDAVSFTVAESNADFREFEFFFFELYPLVPELHVSDDSASAVSFQVTLFPNGG
FCISVNAHHAALDGKTTINFLKSWARTCKNODSFLPQDLIPVYDRTVIRDPMDLDYRI
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SSSYSSSPKELRLSFFV1VYSYALTCLIKARGGDPSRPVGYGFANDVRSLMVSSYSSSPKERLSFFV1VYSYALTCLIKARGGDPSRPVGYGFANDVRSLMVSSSVANDFALVENFTLSFFTLSPGTOVLSVAGSTR
SYFETFWSEEGFLAAARMVSSDSVALIDENVALKIPETLEGFTLLSFTTLSPGTOVLSVAGSTR
FGVYGLLDFGMORPERVVVXSIDOGEAISFABSRAGSGGVELGFELKKHEMDVLVDLLH
                                                                                                                                                                                                                                           /trānslation="MICFILEVESFLVSVSATAPYKDDDVFLINGETDVPFDNHGRT
WTQEEKNILPKNSDNASFSSVVSYKEESGIPQVPYMTARIFRSDFTYSFPVSPGWKFL
RLYFYPTSYRSGFDAVNSFVSVTVNDFTLLQNFSADLTVKASIPESKSLIKEFIVPVY
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QNILLDGNLCPKVSDFGLAKLCEKRESVLSLMDTRGTIGYIAPEVFSRMYGRVSHKSD
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EIAKKMIVVGLWCIQPCPSDRPSMNRVVEMMEGSLDALEIPPKPSMHISTEVITESSS
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17337. .17461,17541. .17640,17803. .17974,18073. .18191,
18285. .18395,18488. .18632,18712. .18844,18934. .19009,
19232. .19297,19385. .19492,19591. .19698,19873. .20070,
20164. .20373)
/note="gene_id:MXF12.6"
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/product="anthocyanin acyltransferase-like protein"
/protein_id="BAB10829.1"
/db_xref="GI:10177550"
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/product="transposase-like protein"
complement(join(30804. .30874,30947. .31289))
/note="contains similarity to Ac-like transposase
                                                                                                                                        /product="receptôr protein kinase-like protein"
/protein_id="BAB10827.1"
/db_xref="G1:10177548"
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/note="gene_id:MXF12.8"
/codon_start=1
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/product="ABC transporter-like protein"
/protein.id="BAB10828.1"
/db_xref="GI:10177549"
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/note="gene_id:MXF12.7"
                                                                                                              /evidence=not_experimental
10819. .13239
/note="gene_id:MXF12.5"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCGCTCGTTATCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACC 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTAAAACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGA 231
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                                                                                                    L.a., and
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llarity 12.4%; Pred. No. 0.0034;
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                           /db_xref-"taxon:32630"
   'organism="synthetic
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Submitted (07.5EP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequenciquences cons.fr - Web : www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum. Saccharomyces extrazzii, zygosaccharomyces arouxii, Saccharomyces servazzii, zygosaccharomyces rouxii, Saccharomyces kluyverii, Kluyveromyces thermotolerans, Kluyveromyces angusta, var. marxianus, Pichia angusta, Debaryones hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                            CNSO6V7I 805 bp DNA STS 11-JAN-2001
T7 end of clone AXOAA017D07 of library AXOAA from strain CBS 7064
of Pichia farinosa, sequence tagged site.
                                                                                                                                                                                       Pichia farinosa.
Pichia farinosa
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durnans, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuvellise, C., Ozier-Kalogeropoulos, O., Pocier, Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of
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de Montigny, J., Spehner, C., Souciet, J., Tekaia, F., Dujon, B., Wincker, P., Artiquenave, F. and Potier, S. Genomic Exploration of the Hemiascomycetous Yeasts: 15. Pichia
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/strain="CBS 7064"
/db_xref="taxon:4920"
/clone="AX0AA017D07"
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38.8%; Pred. No. 0.(
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FEBS Lett. 487 (1), 87-90 (2000)
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/note="end : T7"
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Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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Job time: 11024 sec
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1 (bases 1 to 321003)

8 Moman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.

Direct Submission
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Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN
PRGGRESS ***, in unordered pieces.
                                                   1411 ATGAGTTGCCACTGTTCTATTCTTTAAGTATACCTTTCGACTATGTTTTGAAGATGCAAC 1470
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Dorner,F., Schefflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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Sequence 14 from patent US 5670367.
166494 GI:2724471
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malaria parasite P. falciparum.
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On Aug 24, 1999 this sequence version replaced g1:5731899.

For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82029 CTCCCTATAAATATATATATATATATGATTTATATATGAGCTCATAATATAAATATAAG 82088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1415 GTTGCCACTGTTCTATTCTTTAAGTATACCTTTCGACTATGTTTTGAAGATGCAACGATA 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1235 TACGTCGATTTCTATAAATGCAAGCAAAACATCAGCACAAGATCTTGAAATTGGATTGAG 1294
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                                                                                                                                                                                                                                                                                 phage etc.
Order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Pred. No. 0.092;
0; Mismatches 138; Indels
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Best Local Similarity 49.69
Matches 136; Conservative
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us-08-894-356c-5.rng

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Aromatic acyl tran
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**SIDSI_/gcgdata/geneseq_/geneseq_NAl981.DAT:**

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**SIDSI_/gcgdata/geneseq_/geneseq_NAl983.DAT:**

**SIDSI_/gcgdata/geneseq_/geneseq_NAl983.DAT:**

**SIDSI_/gcgdata/geneseq_/geneseq_NAl985.DAT:**

**SIDSI_/gcgdata/geneseq_/geneseq_NAl986.DAT:**

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**SIDSI_/gcgdata/geneseq_/geneseq_NAl989.DAT:**

**SIDSI_/gcgdata/geneseq_/geneseq_NAl999.DAT:**

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**SIDSI_/gcgdata/geneseq_/geneseq_NAl999.DAT:**

**SIDSI_/gcgdata/geneseq_/geneseq_NAl999.DAT:**
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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                                                                                      OM nucleic - nucleic search, using sw model
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1508
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Aromatic acyl transferase: transformation; anthocyanin pigment; plants; acylation; colour: tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds. /*tag= a /product= Aromatic acyl transferase. Location/Qualifiers 3..1367 cruentus (Clone pCAT8) /*tag= Senecto

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atacaaggotogaaagtttttataaacottogagoottgttggtocoactgataaagtto 720 (first entry) AAAAAAA 1508 aaaaaaa 1508 06-FEB-1997 AAT37308 AAT37308 7 1021 1081 1081 1141 1141 1201 1201 1261 1381 1441 1441 1021 1261 1321 1321 1381 1501 661 721 721 781 781 841 901 901 961 961 1501 RESULT a <u>.</u> g Q g qq q g δ g ŏ δ g Q g ò g ò õ δ δ ò ò ò ŏ à ŏ 음 ö 240 240 300 TCTATGACTITCCACATICTAAATCCCATITCATGGACACTATTGTTCCCAGGCTAAAAC 180 300 CTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATC 360 360 420 420 480 480 540 720 TATCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTCT 120 tctatgactttccacattctaaatcccatttcatcgacactattgttcccaggctaaaac 180 Gaps 9 Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37108-T37313. plants 1 TGAACATTCTCGAACATGCCCGAATATCGCCCCCTCGGGCACCATCGCCATCGCTCGT CTAACACTGATGGTTCGGGTTTTAATAAAAACCCAGAAATAAAACACGTTGAAGGTGATT CTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTAT tgaaagggtggacttcgattattcaatctggtgtagatcggtctttttaacgaaaggat ATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTGATAAAGTTC AATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTC TATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTT TGAAAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTAACGAAAGGAT CTCCACCGGTTTTTGATAGATTGATTAACATCCCACATTTAGATGAAATAAGTTGAGAC ö Length 1508; coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour of flowers Ξ Indels Mizutani BP; 442 A; 294 C; 295 G; 477 T; 0 other; DB 17; 5, Kusumi T,

1140 1320 TIGGIGITGCTGGTACACCTAAGCTCAACTIGTACGACTTTGATTTTGGGTGGGGGAAGC 1200 GCATAAAGTATGAGACTGTTTCAATAGACTATAATACGTCGATTTCTATAAATGCAAGCA 1260 tttctagcatctttgatgaaggattagagagtcaagtttcattgtagatcatcgtcccct 1380 GTAACTGTGGGGCACCATGTGTCCCGACCTTAAAAATGTCGTTTTGACTACGGAAAATG 1020 TCATAATCACCATTGATTGTCGATCTCGTCTTGATCCACCAATTCCCACAGCCTACTTTG 960 **AAGTGCCAAACTTGGAGTACATGTCATCTTTACGGTAACTTGTGGTTATATGGAGTT** GCATAGCGAAATCACTCGTAAAAATAGGAGAAAGAAAGGAGGCGAAGACGAGTTAGAACAGT GGTATGCACTTGGTGCTAAAGTAATTGGAGAGTCTATATGCAAAAATGATATATAATAAGG ggtatgcacttggtgctaaagtaattggagagtctatatgcaaaatgatatataataagg ACGGAATCTTGAAAGATGCCGCGAGATGGCATGAACCTTTCATGATCCCGGCTAGGAAGA AAACATCAGCACAAGATCTTGAAATTGGATTGAGTCTACCGAGTATGCAAATGGAGGCGT TTTCTAGCATCTTTGATGAAGGATTAGAGAGTCAAGTTTCATTGTAGATCATCGTCCCCT TTTTGTGTGTGCATCAAGTTTCTGTCGTTTTTATGAGTTGCCACTGTTCTATTCTTTAAGTA GGTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAAAGAAAAAGGTCTTAACCC Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; scenecio cruentus; Lavandula angustifolia; ds. Aromatic acyl transferase coding sequence BP standard; cDNA to mRNA; 1703

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10; CGTTATCICTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTT 117 144 177 204 237 264 297 357 ATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAAT 417 Gaps 84 TGAACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCA---TCGGCCATCGCT AACAATCTTTATCGGTCACTCTTCAACATTTTTCCCGTTTGCTAGTAATTTGATTGTAT agccctctttgtctctcactctaaaacactaccttccgcttagcggaaatttgttgatgc cgatcaa-----atcgggcgaaatgccgaagtttcagtactcccgtgatgagggcg ATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATATTTGACAGGAAATC actcgataactttgatcgttgcggagtctgaccaggattttgactaccttaaaggtcatc TTCCTAACACTGATGGTTCGGGTTTTAATAAAAACCGGAAAATAAAACACGTTGAAGGTG Ouery Match 13.6%; Score 205.6; DB 17; Length 1703; Best Local Similarity 52.2%; Pred. No. 3.7e-39; Matches 722; Conservative 0; Mismatches 614; Indels 48; 238 265 298 316 358 g 셤 g ò

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AAT37311

RESULT

1035 1095 1161 1275 1335 1047 1107 1221 CAATAGACTATAATACGTCGNTTTCTATAAATGCAAGCAAAACATCAGCACACAGATCTTG 1281 1341 1395 915 975 735 795 867 927 987 atcatcgaacgacgaaaatgagctcgagtacttcagttttacagcggattgccgaggac AGAAAAAGGTCTTAA - - - - CCCAAGTGCCAAACTTGGAGTACATGT - - CATCTTTTACGG agaacaaagtactgaatctcagaggatccgaaccgacaatacgtgtaacgacgttcacaa GTCTTGATCCACCAATTCCCACAGCCTACTTTGGTAACTGTGGGTGCACCATGTGTCCCGAA GAGAGTCTATATGCAAAATGATATAATAAGGACGGAATCTTGAAAGATGCCGCGAGAT ggttatcggaatctaatgga%tcccttcaaaaagatttctcgggattaccggatcgccta AGCTCAACTTGTACGACTTTGATTTTGGGTGGGGGAAGCGCATAAAAGTATGAGACTGTTT catgcaagactataaagtgatcccgctcgtagccgtgcaagtaaccgttttcctaacc CGGGTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCA 556 tgttcatcaatgcttgggcctatattaacaaatttgggaaagacgcggacttgttgtccg AAATAAGTTGAGACATACAAG - - - - GCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTG GTCCCACTGATAAAGTTCGGTCAACGTTTGTGTTGACCCCGAACTAATATCAATCTACTAA TAACTTGTGGTTATATATGGAGTTGCATAGCGAAATCA------CTCGTAAAAATAG CCTTAAAAAATGTCGTTTTGACTACGGAAAATGGGTATGCACTTGGTGCTAAAGTAATTG 1036 aagcaacacataaagagttagttggggataaagggcttcttgttgcagttgcagctattg GG----CATGAACCTTTCATGATCCCGGCTAGGAAGATT----GGTGTTGCTGGTACACCTA ---TATGTGATTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTTCCGGGCT ACTITITIGAAAGGGTGGACPTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTAACGA AAGGATCTCCACCGGTTTTTGATAGATTGATTAACA------TCCCACATTTAGATGA ctgttgattatgcagaattgatttatgtgattcagtccagggattttgaaaaaggtgtgg 1342 GATT 1345 496 535 919 916 1048 1108 1156 1162 1222 1276 703 964 376 418 475 647 763 817 856 868 928 436 qq ò g ò g ò d ò qq ò g à g ò g ò g ò g ò g ò QQ ò g à q ò Op ò ò q ò totectetaaaaeteteataeaettetteeeteteteatgaatttaatetaeeetteate

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                                                                              Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
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                                                                                                                                                                                                                                                                                                                             Mizutani
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                                                                                                                                                                                                                                                                                                                             Kusumi T,
                                                                                                             Scenecio cruentus; Lavandula angustifolia; ds
                                                           Aromatic acyl transferase coding sequence
 BP.
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/product= Aromatic acyl
CDNA to mRNA; 1479
                                                                                                                                                 Location/Qualifiers 3..1343
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                                                                                                                                                                                                                                                                                                                            Fukui Y,
                                                                                                                                Perilla ocimoides (Clone pSAT208).
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95JP-0067159.
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                                        entry)
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                                        (first
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P-PSDB; AAW04725.
 standard;
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AAT37311
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gaaggcgagaaagcaagaaatattgtcgattgatggggagaaatatgcaatgacretttg 1240
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                                                                                                                                                                                                                                                                                            TTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTATATC 484
                                             cccgg------agaaaatgccggagtttcggtatctatccggggactcggt
                                                                                             TGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATCCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.6e-34;
0; Mismatches 657; Indels
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with aromatic acry transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313. NOTE: This sequence is supposed to cross reference with the protein described in AAM04727, however there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide given in the specification and described in AAW04727 that the indexer decided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vectors containing DNA fragments encoding proteins of plant origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tone,
                                                                                                                                                                                                                                  Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1518 BP; 384 A; 340 C; 366 G; 428 T; 0 other;
                   | 1301 ggatgcttttgctgcttatttttcactgggaattaatggttaa 1343
1313 GGAGGCGTTTTCTAGCATCTTTGATGAAGGATTAGAGAGTCAA 1355
                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= Aromatic acyl transferase.
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                                                                                                                                                                                                      Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                                                                Lavandula angustifolia (Clone pLAT21).
                                                                                                        AAT37313 standard; cDNA to mRNA; 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 73-76; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..1355
/*tag= a
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95JP-0067159.
95JP-0196915.
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                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiwara H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUNR ) SUNTORY LTD.
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29-JUN-1995;
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                   CTAACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAACACGTTGAAGGTGATT
                                                                                                                                                                                                                                                              241 tatcgccgg-----agaaaatgccggagttccggtatcagaacggtgact
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 TATCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTTCT
                                                                         TCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                 346 actgctttgcccctagcga@gattatgaagatctccagctgccgccgatagtcgaggaat
                                                                                                                                                  AATC1TTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTC
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TGAACATTCTCGAACATGCCCCAATATCGCCCCCTCGGGCACCATCGGCCATCGCTCGT 60

11.0%; Score 166.6; DB 17; Length 1518; 48.0%; Pred. No. 5.2e-30; Live 0; Mismatches 744; Indels 43;

Query Match 11.(
Best Local Similarity 48.(
Matches 726; Conservative

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WPI; 1996-393401/39.
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                                                                             CTATAAATGCAAGCAAAACATCAGCACAAGATCTTGAAATTGGATTGAGTCTACCGAGTA 1305
                                                                                                                                 1303 aggaattgcaagcttttgatgattattttgcggagggaataaagggttgattaatcattt 1362
                                                                                                                                                                    a-----atcatgtattatgaagttggatgaaatcctctgtttcatctctattgtt 1412
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                        1123 aaaactgttatttctcggtggcgggatcgagcaggcttgatctttacggcgcggattttg
                                                                                                cgttgtgtaaaaccgagggatgctgccggaggattggaggttggattgtctttgccaaagg
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                                                                                                               1306 TGCAAATGGAGGCGTTTTCTAGCATCTTTGATGAAGGATTAGAGGAGTCAAGTTTCATTGT
                                                                                                                                                    AGATCATCGTCCCCTTTTTGTGTGCATCAAGTTTCTGTCGTTTTTATGAGTTGCCACTGT
                                                                                                                                                                                                                                                                                                                                                           Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
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/transl_except= AAT encodes Asp
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/*tag= a
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701..703
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wakan M, Tanaka Y, Yonekura K;
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95JP-0067159.
95JP-0196915.
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17-FEB-1995;
29-JUN-1995;
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                                                                                                                                                                                                                                                                      Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourstions to be produced. Six aspecific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                      plants
tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGATTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTA
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Pred. No. 6e-23;
0; Mismatches 644; Indels 72;
                                                                   coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1622 BP; 478 A; 354 C; 313 G; 477 T; 0 other;
                                                                                                                                                                                                      Claim 4; Page 57-61; 94pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.1%;
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Matches 675; Conservative
P-PSDB; AAW04723
                                                                                                                                          e.g. of flowers
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monitoring gene expression.
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           762 tttctaaagatgaagttcgagccaccttcatcctacaccctattgatatcatgaagctca
                                                           agaaattcatttcgtcaaaaaatcgcaacttaaccggtagtagtaattataatctgtcaa
                                                                                                                                  GAGAAAGAAAGGGCGAAGACG-----AGTTAGAACAGTTCATAATCACCATTGATTGTC
                                                                                                                                                  TCCCGACCTTAAAAAATGTCGTTTTGACTACGGAAAATGGGTATGCACTTGGTGCTAAAG
                                                                                                                                                                                                                                                      tggtgggatcgactcatgagcaacttgtaggaaatgaagggttgtcggtagctgcaaccg
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                                                                                                                                                                                                                                                                                                                                                                                                     1264 CATCAGCACAAGATCTTGAAATTGGATTGAGTCTACCGAGTATGCAAATGGAGGCGTTTT
                                                                                  CTTTTACGGTAACTTGTGGTTATATGGAGTTGCATAGCGAAATCACTCGTAAAAATAG
                                                                                                          ctttcacggtgacatctgcactgatctggacatgcttgtcgaaatcattagacaccgtcg
                                                                                                                                                                                GATCTCGTCTTGATCCACCACTACTTCGCTACTTTGGTAACTGTGGTGCACGTGTG
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                                   AGAAAAAGGTCTTAACCCAAGTGCCAAACTT-
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ВР
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
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Matches 7; Conservative 474; Mismatches
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                         The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having
   AAATTATGTGATTGCGTCACGGTCCCACTTTTTTCACTTCAAGTGACGTTTTTTCCGGGC 473
                                                                                             TCGGGTATATCACTAGGAATGACGAATCATAGCCTTGGTGACGCTAGCACGCGGTTC 533
                                                                                                                            AAAGGATCTCCACCGGTTTTTGATAGATTGATTAACATCCCACATTTAGATGAAAATAAG 653
                                                                                                                                                                                                                                                                                    TIGAGACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTGAT 713
                                                                                                                                                                                                                                                                                                                                                    AAAGTTCGGTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAAAAAGAAAAAGGTC 773
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                                                                                                                                                                                                                                                     Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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AAF58257/c
ID AAF58257 standard; DNA; 936
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                      group; ETM; mismatch; genotyping;
                             Query Match 8.1%; Score 121.6; DB 22;
Best Local Similarity 0.9%; Pred. No. 1.7e-19;
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ID AAF58254 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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1larity 0.9%; Pred. No. 1.7e-19;
Conservative 474; Mismatches 283;
                                             Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
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                            monitoring gene expression.
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group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %; Score 121.6; DB
; Pred. No. 1.7e-19;
474; Mismatches 28
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Best Local Similarity 0.9%;
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294 GGTGATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTATTGACAGGA 353
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                                                                                                       GTATTTCCTAACACTGATGGTTCGGGTTTTAATAAAAAACCAGAAATAAAACACGTTGAA
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7e-19;
es 283; 1
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17-MAR-2000; 2000US-0190259
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Matches 7; Conservative 474; Mismatches 283; Indels
                                                                                                                                                                                                                                                                                         single-nucleotide polymorphisms, e.g. for genotyping
                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                     Seguence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 121.6; ).9%; Pred. No. 1.7e-
                                                                                                                                                                                                Example 6; Page 127; 159pp; English
                                            (CLIN-) CLINICAL MICRO SENSORS INC.
26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                                                         monitoring gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids containing electron-transfer group, useful as labels i
hybridization assays, e.g. for genotyping, allowing repeat analyses
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                                                                                             Electron-transfer group; ETM; mismatch; genotyping;
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Example 6; Page 127; 159pp; English
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CGAAAGGATCTCCACCGGTTTTTGATAGATTGATTAACATCCCACATTTAGATGAAAATA 651
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                                                                                                                                                                                      GAAATCATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAA
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGTGATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAG 351
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                                                                                                                                                                          Score 118.2; DB 22;
Pred. No. 1.1e-18;
59; Mismatches 282;
                                                                                                                                                                                                         Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
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Best Local Similarity
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Example 6; Page 128; 159pp; English.
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411
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                                                                              ETM; mismatch; genotyping;
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59; Mismatches 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
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17-MAR-2000; 2000US-0190259
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                          (first entry)
                                                                           gene expression; ss.
                                                    Oligonucleotide D1954
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a single surface
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AAF58257;
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group, useful as labels in allowing repeat analyses on
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532 TCAACTTTTGAAAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTAA 591
                                                                                                                                                                                                                                                          AGTTGAGACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTG 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping, a single surface
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                                                                                            112 ATCTTTTCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCA 171
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Similarity 0.8%; Pred. No. 1.1e-18;
6; Conservative 469; Mismatches 282; Indels
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Best Local Similarity
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Search completed: November 5, 2001, 18:11:58 Job time: 15453 sec

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(703)683-4109
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                   RESULT
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1691.841 Million cell updates/sec
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Sequence 10, Appl
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-821-994-64
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US-09-247-373B-25
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Sequence
PCT-US93-05000-1
US-08-81-994-59
US-08-171-385-14
US-08-361-441B-14
US-08-985-950-7
US-08-985-950-7
US-08-150-741-1
PCT-US96-12129B-1
US-08-150-741-1
US-08-545-196B-10
US-08-545-196B-10
US-08-545-196B-12
US-08-545-196B-12
US-08-171-385-27
US-08-171-385-27
US-08-171-385-27
US-08-171-385-27
US-08-171-385-27
US-08-171-385-27
US-08-171-385-27
US-08-171-385-27
US-08-171-385-27
      1325
350
350
350
1728
11728
8920
1166
11582
11582
340
340
340
340
332
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ALIGNMENTS

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHETELINGER, F.
APPLICANT: SCHETELINGER, F. G.
TITLE OF INVENTION: RECCMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley 6 Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30472/114 IMMU
                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: APPLICATION NUMBER: EP 91 114 300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 14, Application US/08232463 Patent No. 5670367
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703)836-9300
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                            ACTITICCACATICITAAATCCCATITICATGGACACIATIGITICCCAGGCTAAAACAATCIT 186
                                                                                                                                                                                                                                                                                                                          187 TATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCTAACA 246
                                          Gaps
                                                                                7 TTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGGCCATCGCTCGTTATCTC 66
3.6%; Score 53.6; DB 1; Length 7218; Similarity 1.9%; Pred. No. 0.00017; 5; Conservative 171; Mismatches 90; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Mehta, Kapil
APPLICANT: Mehta, Kapil
TITLE OF INVENTION: Parasitic Nematode Tranglutaminase
TITLE OF INVENTION: Proteins, Nucleic Acid Molecules and
TITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1417 YYYYYYYYYYYYYYYYGTACCAAA 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/781,420
FILING DATE: December 3, 1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                           247 CTGATGGTTCGGGTTTTAATAAAAA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-08-781-420-10
'Sequence 10, Application US/08781420
'Patent No. 6248872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1472 nucleotides
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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2..1105
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                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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; LOCATION:
US-08-781-420-10
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  Query Match
                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Score 47; DB 4; Length 1472;
Pred. No. 0.0048;
0; Mismatches 70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parasitic Nematode Tranglutaminase
Proteins, Nucleic Acid Molecules and
Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 4; Length 147;
Pred. No. 0.0048;
0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,420
FILING DATE: December 3, 1996
                                                                                                                                                                                                                                                    1464 ATGCAACGATATAAAATGAAAAAAAAAAAAAAAAAA 1502
                                                                                                                                                                                                                                                                        ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08781420
Patent No. 6248872
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Mehta, Kapil
ITLE OF INVENTION: Parasitic Nematode
ITLE OF INVENTION: Proteins, Nucleic
ITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: December 3, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/484-9505
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
    3.1%;
56.0%;
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Query Match 3.1%
Best Local Similarity 56.0%
Matches 89; Conservative
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Best Local Similarity 56.04
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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1362 TTGTAGATCATCGTCCCCTTTTTGTGTGCATCAAGTTTCTGTCGTTTTTATGAGTTGCCA 1421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1422 CTGTTCTATTCTTTAAGTATACCTTTCGACTATGTTTTGAAGATGCAACGATATAAAATG 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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;Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.;YOUNG, MARIAN F.;FISHER, LARRY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER:

COMPUTER:

COMPUTER:

COMPUTER:

COMPUTER:

APPLICATION TOWAR:

APPLICATION NUMBER:

CLASSIFICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION TOWARD:

APPLICATION NUMBER:

CLASSIFICATION:

APPLICATION NUMBER:

CLASSIFICATION:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

AND

FILITATION NUMBER:

AND

REFERENCE/POCKET NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

AND

REFERENCE/POCKET NUMBER:

APPLICATION NUMB
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                                                                                                                            GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M
APPLICANT: Girl, Judith G
TITLE OF INVENTION: Interleukin-15 Receptors
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44.6; DB Pred. No. 0.02;
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                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
                                                                   ; Sequence 8, Application US, 08300903A; Patent No. 5591630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-04:0
TELEFAX: 206-587-04:0
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: 3..E
US-08-300-903A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
      RESULT 5
US-08-300-903A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MICROSOft Word for Apple, Version 5.1a
SOFTWARE: MICROSOft Word for Apple, Version 5.1a
APPLICATION NUMBER: US/08/300,903A
FILING DATE: 06-SEPTEMBER-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION OWNER: USSN 08/236,919
FILING DATE: 06-MAY-1994
CLASSIFICATION: 435
APPLICANT: Anderson, Dirk M
APPLICANT: Giri, Judith G
TITLE OF INVENTION: Interleukin-15 Receptors
VINBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1476 AAAATGAAAAAAAAAAAAAAAAAAAAAAAAAA 1508
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NAME: PERKINS, PALFICIA Anne
REGISTRATION NUMBER: 34,695
REFERENCE, POCKET NUMBER: 2822A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-287-0430
TELEFOREX: 206-233-0644
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              Sequence 6, Application US/08300903A Patent No. 5591630 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1534 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101
COMPUTER READABLE FORM:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
COUNTRY: USA
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FEATURE:
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US-08-300-903A-6
                                                                                                                                                                                             US-08-300-903A-6
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2422 AGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTGTTTTAAAATAAGGATTTT 2481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1348 AGAGTCAAGTTTCATTGTAGATCATCGTCCCCTTTTTGTGTGCATCAAGTTTCTGTGTT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42.6; DB 4; Length 2589;
Pred. No. 0.074;
0; Mismatches 74; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                           TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1468 AACGATATAAAATGAAAAAAAAAAAAAAAAAAAAAAA 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
           Goeddel, David v
FRTION: INHIBITORS OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERNCE/DOCKET NUMBER: 4-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,781-1989
TELEPHONE: (415,781-1989
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/569,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.8%;
Best Local Similarity 54.0%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2589 base pairs
                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                            USA
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                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-569-749-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1420 CACTGTTCTATTCTTTAAGTATACCTTTCGACTATGTTTTGAAGATGCAACGATATAAAA 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1345 cattttatgtcactataatcttttgttttttaagttagtgtatattttgttgtggattatc 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1383 TIGIGIGCATCAAGITICIGICGTITITIATGAGITGCCACTGTICTATTCTTTAAGTATA 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROBEY, PAMELA G.
TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS NUMBER OF SEQUENCES: 13 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FILLING DATE: 03-NOV-1989
                                                                                                                                                                                                                                                             Length 1493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTON: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT PPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER APPLICATION NUMBER: 08/924,759
SANTWARE: MICROSOFT WORD VERSION 7.0A
                                                                                                                                                                                                                                                        Score 43.4; DB 6; Length 1
Pred. No. 0.039;
0; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 42.8; DB 3;
58.7%; Pred. No. 0.05;
tive 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1480 TGAAAAAAAAAAAAAAAAAAAAAAAAAAA 1508
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Best Local Similarity 58.7<sup>1</sup>
Matches 74; Conservative
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Best Local Similarity 55.7
Matches 83; Conservative
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APPLICANT: Rothe, Mike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1503 AAAAAA 1508
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                                                                                                                                  ; SEQ ID NO:5:
: LENGTH: 1493
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US-09-248-335-35
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LENGTH: 1098
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US-08-569-749-1
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1406 TTTTTATGAGTTGCCACTGTTCTATTCTTTAAGTATACCTTTCGACTATGTTTTGAAGAT 1465
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                                                                                                                                                                                                                                                                                                                                                                                       Score 42.2; DB 3; Length I'
Pred. No. 0.074;
O. Wismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-821-994-64
Sequence 64, Application US,08821994A
Patent No. 6226643
GENERAL INFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
TITLE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-12
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1996-03-22
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.8%;
Best Local Similarity 63.1%;
Matches 65; Conservative
                              INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-994-64
                                                                                                                                                                                                                   CDS
55..1223
                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
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LOCATION:
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; LOCATION:
US-09-154-874-4
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LENGTH: 1474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US96/12860

FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
ATORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REFERENCE/DOCKET NUMBER: 24,774
REFERENCE/DOCKET NUMBER: 24,774
REFERENCE/DOCKET NUMBER: 24,774
REFERENCE/OFFICE NUMBER: 415,781-1989
TELEPHONE: (415)781-1989
TELEFAX: (415)781-1989
STELEFAX: (415)398-3249
STELEFAX: CARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.8%; Score 42.6; DB 5; Length 2589; Best Local Similarity 54.0%; Pred. No. 0.074; Matches 87; Conservative 0; Mismatches 74; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: FADER, GARY MICHAEL
TITLE OF INVENTION: ISOFLAVONE BIOSYNTHETIC ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERNCE/DOCKET NUMBER: BB-1098-A
TELECOMMUNICATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/931,668
FILING DATE: SEPTEMBER 17, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09154874
Patent No. 6054636
                                                                                                                                                                                                                                                                                                                                              LENGTH: 2589 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US96-12860-1
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DB 4; Length 991;

Score 41.8; DB 4; Length 9 Pred. No. 0.087; 0; Mismatches 47; Indels

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1392 TCAAGTTTCTGTCGTTTTTATGAGTTGCCACTGTTCTATTCTTTAAGTATACCTTTCGAC 1451
                                                                                                                                                                                                                                                                                                                                       861 ttaattgactgtgatttggttgggtattggctattttaattttaactaaaaaagtgttc 920
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 991
                                                                                                                                                                                                               2.8%;
                                                                                                                                                                                                                                   Best_Local Similarity 59.8
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; IMMEDIATE SOURCE:
; CLONE: SSM.PK0067.GS
US-09-296-715-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1007 MARK CITY: WILMINGTON STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                              ; ORGANISM: SOYBEAN US-09-247-373B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
TISSUE TYPE:
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US-09-296-715-25
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                                                                                                          TYPE: DNA
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                       Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              861 TTAATTGACTGTGATTTGGTTGGGTATTGGCTATTTTAATTTTAACTAAAAAAAGTGTTC 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Petent NO. 6168954
GENERAL INFORMATION:
APPLICANT: WCGONIGLE, BRIAN
APPLICANT: WCGONIGLE, BRIAN
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILLING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.8%; Score 41.8; DB 3; Length 991;
59.8%; Pred. No. 0.087;
tive 0; Mismatches 47; Indels
                                                                            APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: BAXYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. DU FONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
                                                                                                                                                                                                                                                                                                                              COMPUTER EADBABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CL-1108
               Sequence 25, Application US/08924747
Patent No. 6063570
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOOY, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/POCKET NUMBER: CL-1:
TELEPHONE: 302-992-9112
TELEPHONE: 302-773-0164
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGRE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: NUCLEIC CLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IMMEDIATE SOURCE:
; CLONE: SSM.PK0067.G5
US-08-924-747-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: S
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US-09-247-373B-25
  US-08-924-747-25
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DB 4; Length 991;
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANTEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: ENTYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/296,715
                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.8%; Score 41.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CL-1108
                                                                                                                                           ; Sequence 25, Application US/09296715; Patent No. 6171839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFRENCE/DOCKET NUMBER: CL-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 991 base pairs
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us-08-894-356c-5.rni

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| Sequence 4, Application US/08897340 |
| Sequence 4, Application US/08897340 |
| Sequence 4, Application US/08897340 |
| Septent No. 5955306 |
| GENERAL INFORMATION: Weight Control Pathway Genes and Uses TITLE OF INVERTION: Therefor |
| TITLE OF INVERTION: Therefor |
| UMBER OF SEQUENCES: 36 |
| CORRESPENDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD, LLP |
| STRRET: Boston |
| STRRET: Boston |
| STRRET: Massachusetts |
| COUNTRY: USA |
| 102109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 41.8; DB 2; Length 1700;
66.3%; Pred. No. 0.1;
tive 3; Mismatches 25; Indels 0
59.8%; Pred. No. 0.087; ative 0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,340
FILING DATE: US/08/897,340
FILING PAPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/715,032
FILING DATE: 17-SEP-1996
ATTORNEY/AGENT INFORMATION:
MANDE: GILOST TOAN
MANDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/POCKET NUMBER: MNI-005CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1486 AAAAAAAAAAAAAAAAAAA 1508
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Best Local Similarity 66.3%
Matches 55; Conservative
    Best Local Similarity 59.8%
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE:
US-08-897-340-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
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Search completed: November 5, 2001, 18:04:56 Job time: 15096 sec

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em_esthum13:*
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em_esthum24:*
em_esthum26:*

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(without alignments)
2450.648 Million cell updates/sec
                                                            November 5, 2001, 18:00:56 ; Search time 5816.79 Seconds
                                                                                                                  20456230
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                      10228115 seqs, 4726426750 residues
                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                    Scoring table:
                                                                                                                                                                      Database :
                                                                           Sequence:
                                                                                                      Searched:
                                       Run on:
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em_estpl5:*
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em_estpl7:*
em_estpl8:*
em_estpl8:*

em_estov2:*
em_estpl1:*
em_estpl3:*

em_estpl3:* em_estpl4:*

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em_estro4::*
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em_estro13:*
em_estro14:*

em_estrol1:*

em_estro15:*
em_estro17:*
em_estro13:*

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gb_est25:*

gb_est25:*

gb_est28:*

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gb_est30:*

gb_est31:*

gb_est41:*

gb_est41:*

gb_est44:*

gb_est44:*

gb_est46:*

gb_est46:*

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em_gss_pro:* em_gss_rod1:* em_gss_rod2:* em_gss_rod3:*

em_gss_rod4:: em_gss_rod5:: em_gss_vrt1:: em_gss_vrt2:: em_gss_vrt3:: gb_gss1:: gb_gss1::

gb_gss4:* gb_gss5:* gb_gss6:*

gb_gssll:* gb_gssl2:* gb_gssl3:*

gb_gss14: gb_gss15: gb_gss16:

gb_gss17: gb_gss18: gb_gss19:

gb_gss20: gb_gss21: gb_gss22:

gb_gss24: gb_gss25: gb_gss26: gb_gss23

gb_gss27

gb_gss7: *
gb_gss8: *
gb_gss9: *
gb_gss10:

em_gss_inv1:* em_gss_inv2:* em_gss_inv3:*

em_gss_hum6:* em_gss_hum7:* em_gss_hum8:* em_gss_hum9:*

em_gss_fun:*
em_gss_hum1:*
em_gss_hum2:*

gb_est110:*
gb_est111:*
gb_htc:*

em_gss_hum3:* em_gss_hum4:* em_gss_hum5:*

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gb_est48:*

gb_est49:*

gb_est50:*

gb_est51:*

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em_estro21:*
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em_estro23:*
em_tc:*
gb_est107:*
gb_est108:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 9b-9ss31:* 9b-9ss32:* 9b-9ss34:* em_9ss_rod6:* em_9ss_rod6:* em_9ss_rod7:* em_9ss_rod8:* 9b-9ss35:* 9b-9ss35:*

gb_gss28:* gb_gss29:* gb_gss30:*

JOURNAL Unpublished (2000) COMMENT Contact: Cathy Ronning The Institute for Genomic Research For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com	Seq primer: M13F-R. Location/Qualifiers 1. 690 Norganism="Solanum tuberosum"	ry Match tt Local Similari ches 316; Cons 21 CGAATATCGC 2	OY 141 AAATCCCATTCATGGACACTATTGTTCCCAGGGTAAAACAATCTTTATCGGTCACTCTT 200 119 AAACCCGATTTCGTTCAAAACATTATTCCTCCTCTTAAAAATTCACTCTCCTC	381 TATCACTTGACCTCATTGGGAATGCAATCAGTGGTGGGTCGGTC
SUMMARIES Query re Match Length DB ID Description	.2 8.6 690 155 BG59947 .4 8.2 763 155 BG59947 .4 8.2 763 155 BG591758 .4 7.7 570 142 BB292784 .8 EB192784 BES7429600 .6 7.1 575 142 BE920784 .8 EB1920784 BE920786 .8 FILE AW216206 .9 7.1 606 113 AW216206 .9 7.1 608 173 BG097054 .4 6.9 593 113 BA221076 .5 564 142 BE922776 .5 564 142 BE92176 .6 511 482 182176 .6 51 482 1842 BE92178 .6 6.1 482 144 BF92178 .6 6.1 482 144 BF92178 .6 6.1 482 144 BF92178 .6 6.1 482 144 BF93178 .7 6 6.1 482 144 BF93178 .8 659 155 BG581249 .8 659 155 BG58124 .8 659 155 BG581249	5.7 403 143 BF055202 BF053202 5.6 542 167 BE436185 BE436185 5.6 518 119 AW55280 AW550185 5.4 783 155 BE684708 BC584708 5.4 708 138 BE660849 BE65084708 5.3 676 153 BC455847 BC455847 5.3 648 154 BC457806 BC457807 5.2 408 151 BF648786 BC457806 BC445807 5.2 642 153 BC441805 BC448105 BC448105 5.1 603 118 AW616119 BF642724 4.9 654 151 BC442724 BF642724	4.9 630 118 AW885227 4.8 597 120 AW774948 4.7 605 30 AV440958 4.7 694 117 AW860686 4.7 694 117 AW860686 4.7 829 155 BG284678 4.7 414 142 BE921378 4.7 414 18 BE921952 4.5 433 120 AW756036 4.2 366 142 BE920010 4.1 456 142 BE923572	BG599447 690 bp mRNA EST 12-APR-2001 EST504342 cSTS Solanum tuberosum cDNA clone cSTS25122 5' sequence, BG599447 BG599447 EST. BG599447 EST. FOLANT GI:13616583 EST. FOLANT CI:13616583 EST. FOLANT CI:13616583 EST. FOLANT CI:13616583 EST. FOLANT COLOR CO
Result No. Scor	2 124.4 3 116.4 4 4 110.2 5 107.6 6 107.5 9 103.4 11 103.2 11 103.2 11 99.2 11 91.6 11 91.6 11 91.6 11 91.6 11 91.6 11 91.6	18 85.8 20 84.6 21 82.6 22 82.6 24 80.5 25 79.4 27 79.2 28 78.8 26 79.4 27 79.2 28 78.8 29 78.8 50 76.6		RESULT 1 B6539947 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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SOURCE
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BG591758 763 bp mRNA EST 12-APR-2001
EST499600 P. infestans-challenged leaf Solanum tuberosum cDNA clone
BPLI10A14 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: Baluescript SK(-); Site_1: EcoRI; Site_2: Shori; Whole plants were challenged with 450,000 sporanjadml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen inmediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that than sociated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sateridae; euasteridas; Solanaceae; Solanum.

(bases 1 to 763)

Zhang, P., Hernandez, M., Tornqvist, C.-E, Wirtz, U., Loukoianov, A., Rangel, P., Haberlach, G.T., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.M., Helgeson, J. and Baker, B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Incompatible Reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTTACTTATTTTGATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGATATTATTCT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAAT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAAGCTCCCCATTTCCAAACCCGATTTCGTTCAAAACATTATTCCTACTCTTAAAAATT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 ACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAAACACGTTGAAGGTGATTCTG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 GAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGTG 423
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%; Score 124.4; DB 155; Length 763; 53.2%; Pred. No. 1.5e-19; 1ve 0; Mismatches 246; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="P. infestans-challenged leaf"
/tissue_type="leaf"
/dev_stage="6 week old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="BPL110A14"
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                                                                                       BG591758.1 GI:13609898
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162 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 297; Conservative
                                                                                                                                                            Solanum tuberosum
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KEYWORDS
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and perilized freely. The tissue was immediately frozen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryote, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 57);
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of ESTs from potato leaves and petioles
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potato leaves and petioles Solanum tuberosum cDNA clone
GGGTCCAATTAGCTCCGGTCTTAGCCATTCAAGTGACACTTTTTCCGAATCTTGGTGTT 452
                                                                                                                                                                           484 CACTAGGAATGACGAATCATAGCCTTGGTGACGCTAGCACGCGGGTTCAACTTTTTGA 543
                                                                                                                                                                                                                             453 CCATTGGTTTCACTAACCATGATGTTGTTGGTGGAGCTACCATAGTAGGGTTCATTA 512
                                                                                                                                                                                                                                                                               544 AAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGAAAGGATCTC 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cathy Rouning
The Institute for Genomic Research
For clone request: please contact Research Genetics,
Division Let 1-800-711-6195, email cdna@resgen.com.
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/clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
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/organism="Solanum tuberosum"
/cullivar="Kennebec"
/db_xref="taxon:4113"
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Kosidae; eurosida: Fabales; Fabaceae; Papilionoideae; Medicago.
1 (bases 1 to 788)
VandemBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
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TCTTACTTATTTTGATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGATATTATTCTA 151
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Contact: VandenBosch K
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                                    TGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAATC
                                                       185 TITAICGGICACICITCAACAITITITCCCGITTGCTAGTAATITGAITGTAITICCIAA
                                                                                                                                         212 ACTCTCCCTCACTCTCAAACACTATACGCCCTTAGCTGGAAACGTTGCTCGTCCACTAGA
                                                                                                                                                                                                            272 TACAAACGG------ATATCCTGAGTTACATTATGTGACAGGAGATTCTGT
                                                                                                                                                                                                                                                TGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATCCTCG
                                                                                                                                                                                                                                                                 317 ATCTGTTACTTTTTCTGAGACTGATATGGATTTCAATTGTATCTCATTGGTGACCATCCGCG
                                                                                                                                                                                                                                                                                                                        AAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGTGA
                                                                                                                                                                          CACTGATGGTTCGGGTTTTAATAAAAACCCAGAAATAAAACACGTTGAAGGTGATTCTGT
                                                                                                                                                                                                                                                                                                                                                                                            TTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTATATC
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EST335180 KVO Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
1. 788
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/cultivar="genctype A17"
/db_xref="taxon:3880"
/clone="gKV0-1613"
/clone_lib="KV0"
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Texas A&M University
College Station, TX 77843-3258, USA
TTE: 409 845 7707
Fax: 409 845 2891
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Texas A&W University name:T260795e
TICR sequence name:MTGAU50TK
More information is available at.
http://chrysie.tamu.edu/medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
BE187619
BE187619.1 GI:8666803
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RESULT

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/tissue_type="Seedling roots"
//de_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
//dab_host="E.coli strain xLOLR"
//dab_host="E.coli strain xLOLR"
//note="Vector: pBluescript SK -; Site_l: EcoRI; Site_2:
Xhoi: JONA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

188 c 100 g 262 t l others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A EST 02-OCT-2000 petioles Solanum tuberosum cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 ------CGTTCCCTCGCTTGATCTAACCGAACCTCAACTCGAATTTACTCTTAAC 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 TACTCAAGAGATGTTAATGATTCCACCCTTTGGTACCAAAGTTGCAACA---AATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 AAACAATCTTTATCGGTCACTCTTCAACATTTTTCCCGTTTGCTAGTAATTTGATTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 TTTCCTAACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAACACGTTGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 110.2; DB 164; Length 788;
Pred. No. 3.9e-16;
0; Mismatches 213; Indels 21;
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EST424237 potato leaves and petiole
cSTB6C8 5' sequence, mRNA sequence.
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Lycopersicon hirsutum
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KEYWORDS
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                                                                                                                                                                                                                                   /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in
                                                                                                                                                                                                                                                                                                                                                                                                                 3,
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                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                    DB 142; Length 575;
 Generation of ESTs from potato leaves and petioles Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Score 107.6; DB 142; Length
Pred. No. 1.6e-15;
0; Mismatches 239; Indels
                                                                                                                             /cultivar="kennebec"
/db_xref="taxon:4113"
/clone="cSTB6C8"
/clone=lb="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                    /organism-"Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                                                                                       139 g
                                                                                                                                                                                                                                                                                                           liquid nitrogen
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53.88;
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Best Local Similarity 53.8
Matches 299; Conservative
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1 (bases 1 to 487)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
,F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tankaley, S.D.
Generation of ESTs from wild tomato (Lycopersicon hirsutum)
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/db_xref="taxon:62890"
/clone="ccHTID15"
/clone=lib="L. hirsutum trichome, Cornell University"
/clone_lib="L. hirsutum trichome, Cornell University"
/clssue_type="trichome"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded mixture of cells which is highly enriched for trichome likely with minor contaminations of other types of leaf cells"
                                                                                                                                                                                                                                                                                           Embryophyta; Tracheophyta;
EST307245 L. hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHT1D15 5', mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: David Frisch
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon hirsutum"
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/cultivar="TA496"
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/color="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: EcoR1; EcoR1;
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Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots;
Asteridae: euasterids I; Solanales; Solanaceae: Solanum;
                                                                                                                                                                                                                                  AW221049 606 bp mRNA EST 07-DEC-1999
SET297318 tomato fruit mature green, TAMU Lycopersicon esculentum
CDNA clone cLEF3F1, mRNA sequence.
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Pred. No. 2.2e-15;
0; Mismatches 280;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
TTE: 864 656 4366
Fax: 864 656 4293
                                                                                                              441 CCATTGGTTTCACTAACCATGATGTTGTTGTGGTGATG 476
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Best Local Similarity 50.4%;
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E 1 (bases 1 to 508)
S van der Hoeven, R. S., Bezzeridae, J., Holt, I. E., Liang, F., Cho, J., Utterback, T., Hansen, C. L., Doan, B., Bougri, O., Buell, C. R., Ronning, C. M., Fry, W. E., Tanksley, S. D. and Baker, B.

C Marchished (2000)
C Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: plasse contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@fessgen.com.
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/clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
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1 (bases 1 to 574)
Van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leafletts and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE922746 574 bp mRNA EST 02-OCT-2000 EST426515 potato leaves and petioles Solanum tuberosum cDNA clone cSTB21L12 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                  335
                                                                                                                                                                                                                                                                                                                                                                                                                                    477
                               CGTTATCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTT 117
                                                                                                TCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAA 177
                                                                                                                                                                  AACAATCTTTATCGGTCACTCTTCAACATTTTTCCCGTTTGCTAGTAATTTGATTGTAT 237
                                                                                                                                                                                              171 AACATTCACTCTCCCTCACTCTCAAACACTACACCCCTTAGCTGGCAACATTGCTTGTC 230
                                                                                                                                                                                                                                238 TTCCTAACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAACACGTTGAAGGTG 297
                                                                                                                                                                                                                                                                                                  ATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATC 357
                                                                                                                                                                                                                                                                                                                                                                    ATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAAT 417
 Gaps
                                                                                                                                                                                                                                                                 CACTAAATTCGAGTGGTT-------ATCCTGAGTTGCGTTATGTGACTGGAG
                                                                                                                                                                                                                                                                                                                     396 CACCGGGGGTCAAACTAGTCCCGGTCTTAGCCATTCAAGTGACACTTTTTCCGAATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGTGATTGCGTCACGGTCCCACTTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGG
 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCAC 526
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          petioles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="potato leaves and petiole/thisbue_type="leaflets and petioles" /dev_stage="8 weeks old plants" /lab_host="SOLR"
Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="cSTB21L12"
ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE922746
BE922746.1 GI:10448822
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potato.
Solanum tuberosum
252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                               118
                                                                                                                                                                178
                                                                                                                                                                                                                                                                                                                                 276
                                                                                                                                                                                                                                                                                                                                                                  358
                                                                                                                                                                                                                                                                                                                                                                                                                                    418
 Matches
                                                                51
                                                                                                                                                                                                                                                                 231
                                                                                                                                                                                                                                                                                                  298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478
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KEYWORDS
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum
Makaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST297519 tomato fruit mature green, TAMU Lycopersicon esculentum
                                                                                                                                                                                                                                                                            TTTTCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGATTCTATATCTGTTACTTTTATTGAGACTGATATGAATTTCAATCATCTCATTGGTA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 ATCATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTATGTGATTGCGTCACGGTCCCACTTTTTTCACTTCAAGTGACGTTTTTTTCCGGGCT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGGTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 TIGGCATATCCGTIGGITITAGTAACCATCATGTCGCTTGTGAAGGAAATACCAICGTGA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTITITGAAAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTCATAAGAACATGGGGTTTACTCCAACAATTCGGCGGTGATGAACAGTGCTTAGAGA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAAACAATCTTTATCGGTCACTCTTCAACATTTTTTTCCCGTTTGCTAGTAATTTGATTG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 GTCCACTAAATTCGAGTGGTT------ATCCTGAGTTGCGTTATGTGACTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGGATCTCCACCGGTTTTTGATAGATTGATTAACATCCCACATTTAGATGAAATAAGT 654
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                 23 TTTTATTCTACAAGCTACCAATTTCCAAACTCGATTTCGTTCAAACCATTATTCCTACTC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTTCCTAACACTGATGGTTCGGGTTTTTAATAAAAACCAGAAATAAAACACGTTGAAG
                                                                                                                                                                                                           18;
                                                                                                                                      Length 574;
                                                                                                                                  Score 103.4; DB 142; Lengt
Pred. No. 1.6e-14;
0; Mismatches 241; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
183
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AW221050
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1 (bases 1 to 591)
Jaclash, Verballov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
                                                                                                                    Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
EST405335 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG15H6, mRNA sequence.
BE414257
BE434257.1 GI:9432100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         locules were discarded prior to freezing the pericarp." 129\ c 121\ g 182\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TITTCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCAGGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 TTAAAAATTCACTCTCCCTCACTCTCAAACACTATACGCCCTTAGCCGGAAACGTTGCTT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 GTCCACTAGATACAAACGGAT ------ATCCTGAGTTACGTTATGTGACAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 ATCATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 TATTATTTTACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAAAACATTATTCCTCCTC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                         Spermatophyta; Maynoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAAACAATCTTTATCGGTCNCTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation of EST: from tomato fruit tissue, breaker stage Unpublished (2000)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 TATTTCCTAACACTGATGGTTCGGGTTTTAATAAAAAACCAGAAATAAAAACGCTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCATCCGCGTAAGGCTTTTTTTTTTCACTTTGTTCCTAAGTTAGGGGAACCTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_nost="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99; DB 167;
Pred. No. 1.8e-13;
                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tal: 864 656 436
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4081"
/clone="cLEG15H6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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illarity 51.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prime sequence.
                                                                                                                                                                                                  Lycopersicon.
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Best Local Similarity
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                                                                                                    tomato.
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  DEFINITION
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JOURNAL
COMMENT
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                                    ACCESSION
                                                           VERSION
KEYWORDS
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                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                            /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTTCTTC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATGACTITCCACATICTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 TACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAAAACATTATTCCTCCTCTTAAAAT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 TCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 GIGICIGITACTITITICGAGACTGATATGAATTTCAATTATCTCATTGGTGACCATCCG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AACATTCTCGAACATGCCCGAATATCGCCCCCTCGGGCACCATCGGCCATCGCTTTA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 GATACAAACGGAT------ATCCTGAGTTACGTTATGTGACAGGAGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 GTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 CGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGT
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                                                                                                                                                                       /db_xref="taxon:4081"
/clone="CLEF3F3"
/clone="Lb="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 113; Length 583;
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                                                                                                                  1. .583
/organism="Lycopersicon
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                                                                                                Location/Qualifiers
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                Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                       /cultivar-"TA496"
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Generation of ESTs from potato leaves and petioles
Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Asteridae: euasterids I; Solanales: Solanaceae: Solanum.

1 (bases 1 to 564)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564~\rm bp mRNA EST 02\text{-}OCT\text{-}2000 potato leaves and petioles Solanum tuberosum cDNA clone 5' sequence, mRNA sequence.
                                    118 TCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 CGGGTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCA 534
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                                                                                                                               535 ACTITITGAAAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib-"potato leaves and petioles"
/tissue_type-"leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_nost="SOLR"
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB13B18"
                                                                                                                                                                                                                                                               595 AAGGATCTCCACCGGTTTTTGATAGAT 621
                                                                                                                                                                                                                                                                                                    liquid nitrogen.
139 c 97
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AUTHORS
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/note="Vector: pBluescriptSKmCUdadpt; Site_1: 5' EcoRI; Site_2: 3' XhoI; Roots were harvested from plants grown under the following deficiencies/stresses: 10 mM Al, Zn, P, K, Fe,N. mRNA was isolated from indivdual treatments. Proportional aliquots of mRNA of each treatment were mixed and used for library construction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           To faces 1 to 482)

Van der Hoeven, R.S., Garvin, D.F., Matern, A.L., Holt, I.E., Liang, F.,
Upton, J., Hansen, T.S., Ronning, C.M., Craven, M.B., Bowman, C.L.,
and Tanksley, S.D.
Generation of ESTs from tomato nutrient-deficient roots
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST400516 tomato nutrient deficient roots Lycopersicon esculentum cDNA clone cLEW18020 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                     359 ATCCTCGAAATGCTAAGGATTTTTATCCCATT---CCTCAATTGGCACAACCTAAGGATG 415
                                                                                                                                                                                                    358 ATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAAT 417
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------ATCCTGAGTTGCGTTATGTGACTGGAG
                                                                   ATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTGACAGGAAATC
                                                                                                                                299 ATTCTATATCTGTTACTTTATTGAGACTGATATGAATTTCAATCATCTCATTGGTAACC
                                                                                                                                                                                                                                                                                                                                                               478 GTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACT
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/tissue_type="roots"
/dev_stage="5-6 weeks old"
/lab_host="SoLR"
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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/clone="cLEW18020"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538 TTTTGAAAGGGTGGACTT 555
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DB 144; Length 482;

Score 92.6;

6.1%;

5

g ò d õ g õ g ò q ò g ò g ò g

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/dev_stage="effective root nodules harvested one month post inoculation with Sinorhizoblum melilot!"
//lab_host="E. col! strain xXOLR"
//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhoi; cNNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizoblum meliloti. The cDNA was directionally ligated into the Uni-zAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 497)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Llang, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW930934 497 bp mRNA EST 30-MAY-2000 EST356777 tomato fruit mature green, TAMU Lycopersicon esculentum cDNA clone cLEF42M23 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                Length 630;
                                                                                                                                                                                                                                                                                                                                            Score 91.4; DB 155; Length
Pred. No. 1.2e-11;
0; Mismatches 201; Indels
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llarity 53.1%;
Conservative (
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Best Local S
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Sosidae; eurosida; Fabales; Fabaceae; Papilionoideae; Medicago.
1 (bases 1 to 630)
Fedorova,M., Plerson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town
.C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
ESTS from one month old nitrogen-fixing root nodules of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Minnesota name: M382308e TIGR sequence name: MTCDG96TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG581249 630 bp mRNA EST 11-APR-2001
EST482982 GVN Medicago truncatula cDNA clone pGVN-64023 5' end,
                                                                    CICTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTTCTTCT 123
                                                                                                           CTCTTACTTATTTTGACCATGTTTGGTTAGGGTTTCGCCGTATGAGGCGGATATTTT 109
                                                                                                                                                     124 ATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAAT 183
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Unpublished (2001)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 1
Tel: 612 655 5715
Fax: 651-649-5058
                              Gaps
                                                                                                                                                                                                                                           CTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 GGGTCCAACTAGCCCGCTCTTAGCCATTCAGGTGACACTTTTCCGAATCTTGGTGTAT
                              15;
                              Indels
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/clone_lib="GVN"
/tissue_type="N2-fixing root nodules"
      Pred. No. 6.2e-12;
0; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATTGGTTCACTAACCATCAT 477
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BG581249
BG581249.1 GI:13596313
      52.8%;
                            Matches 234; Conservative
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Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; cLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 CCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGTGATTGCGTCACGGTCCCCACTT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 TTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTATATCACTAGGAATGACGAATCAT 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 89.2; DB 122; Length 497; 53.1%; Pred. No. 4.1e-11; tive 0; Mismatches 168; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
                                                                                                                                                                                                                                                                                       /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEF42M23"
                                                                                               Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4293 Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 t
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1. .497
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                                                          Unpublished (1999)
Contact: David Frisch
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106 c
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Matches 190; Conservative
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gb_sts2:" gb_sts3:"

gb_sy:*

gb_vi2:*

Searched:

Sequence:

Run on:

gb_sts1:"

em_vi:*

em_sy:* em_un:*

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em_pat:

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November 5, 2001, 16:54:14; Search time 8904.87 Seconds (without alignments) 2643.712 Million cell updates/sec
                                                                                                           US-08-894-356C-6
1522
1 NTGACCACCTCGAATC.....TTTTTTTTTTTTTTTTTTT 1522
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                      1344157 segs, 7733874588 residues
                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_htgo_hum: *
em_htgo_lum: *
em_htgo_rod: *
em_htgo_lum: *
em_htg_hum: *
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em_hum1:*
em_hum2:*
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Maximum DB seq length: 200000000
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gb_ba2:*
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                                                                                                                                                         Scoring table:
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gb_htg22:* gb_htg23:* gb_htg24:* gb_htg25:*

gb_pr1:* gb_pr2:* gb_pr3:*

9b_htg15:*
9b_htg16:*
9b_htg17:*
9b_htg18:*
9b_htg18:*

gb_htg14:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 9b_pr8:* 9b_pr9:* 9b_ro1:* 9b_ro2:* 9b_in4:* em_ba3:*

SUMMARIES

		c1	44	Ø	rı	ru	ri	æ	SQ
		E12756 Perilla oci	rilla	entian	tanat	cto c	E12754 Gentlanatri	AB026494 Gentiana	abido
t to		Peri	40 Pe	08 Ge	Gent	Sene	Gent	94 Ge	92 AI
Description		12756	B0293	B0107	12753	12757	12754	B0264	B0168
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uery		50.3	50.2	12.7	12.7	11.3	10.1	10.1	7.0
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Score		765.4	763.	19	19	172.	153.	153.	106.
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(C12N9/10,C12R1:19); strandedness: Double; topology: Linear; Kev

8558 E

C12R1:865)

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301 CAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCCGTTAGGC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCTTTTCACCCAATCTGAAATTAAGAAATTGAAGGGTTTGATTCAGAGAAAAGCCCCAA 787
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 FT
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                                                                                                                                                   others
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                                                              /product='acyltransferase'
                                                                                                                                                                                                                Score 765.4; DB 10;
Pred. No. 2.5e-147;
1; Mismatches 417;
/organism='Perilla
                                /clone='psar208
                                                                                                                                                 411
                                                                               Location/Qualifiers
1. 1479
/organism="unidentified"
                                                                                                                               /db_xref="taxon:32644"
316 c 331 g
                                                  . .1343
                /tissue_type='leaves
                                                                                                                                                                                                              Query Match 50.3%;
Best Local Similarity 71.1%;
Matches 1056; Conservative 1
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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Perilla frutescens leaf cDNA to mRNA.
Perilla frutescens leaf cDNA to mRNA.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB029340 1476 bp mRNA PLN 04-APR-2000
Perilla frutescens mRNA for anthocyanin acyltransferase, partial
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                                                                                             CGTTTGCGATGGCGAAGATCCTGCGGGGGTTTGGTCGGAGATGAAGGGGTGTTTGGG 1027
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                                                                                                                                                                                                                                                        1135 CAGGATCGAGCAAGCTAGATCTTTACGGTGCAGATTTTGGATGGGGGAAGCCGAGAAAGC 1194
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907
                                              196
                                                                     954
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CAGCTGAGGCGATCGCGGGGAAATAGAGAAGAGGACGAGGACGAGAAGATTCTAGAAA
                                                                                                                                                                                                        CGGTGGAGAAATGGTCGCCGGAGATTCGTAAAGCGTTGCAGAAATCATATTTTCGGTGG
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                                              TCGATTTAAGGCCGCGTTTGGATCCGCCGGCTCCGGGGAACTACTTCGGAAACTGTCTAT
                                                                                                                                                                                           CTGTGGAGAACTGGCCGTCTGAGATTCGCGAAGCCTTGCAAAACTGTTATTTCTCGGTGG
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AB029340.1 GI:7415645
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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/Translation="VIECRNCPPPDSVAEQSVPLTFFDMTWLHFHPMLQLLFYEFPC
SKQHFSESIVEKLGSLSKTLIHFFPLSCNLITPSSPEKMPERFYLSGDSVSFTIAES
SDDFDDLVGNRPESPVRINTNVPKLPPLYESDRKLEQVFAUQYTFPGRGVGIGTAT
HHTVSDAESFLARITHRYPTRENDEDEEFKSLPVFDRSVIKYPTKFDSITWRNA
LKFPLQSRHPSLPTDRIRTTFVFTQSKIKKLKGWIQSRVPSLVHLSSFVAIAAYWARG
ITKSFTADEDQDNEDAFFLIPVDLRPRLDPPVPENYFGNCLSYALPRHRRELVGEKG
VFLAAEVITAAEIKKRINDFRKILETVEKMSPEIRKALQKSYFSVAGSSKLDLYGADFGW
GRARKOBILSIDGSKAMTLCKARDFEGGLEVCLSLFKDKMDAFAAVFSLGING"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 429; Indels
                                                                                                                                                /product="anthocyanin acyltransferase"
/protein_id="BAA93475.1"
/db_xref="GI:7415646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.2%; Score 763.6; DB 12; 70.5%; Pred. No. 6e-147;
                                       /organism="Perilla frutescens"
/db_xref="taxon:48386"
/tissue_type="leaf"
Location/Qualifiers
                                                                                                                                /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 1047; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; 1 to 1679)

Fujiwara, H., Tanaka, Y. and Kusumi, T. Eujiwara, H., Tanaka, Y. and Kusumi, T. Eujiwara, Submission
Submitted (22-300)
Submitted (22-300) to the DDBJ/EMBL/GenBank databases. Hiroyuki Fujiwara, Suntory LTD., Inst. of Fundamental Research; 1-1-1, Wakayamadai, Shamamoto-cho, Osaka 618-0024, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA PLN 20-FEB-1999
for Anthocyanin 5-aromatic acyltransferase,
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                                 TCGTTTTCACCCAATCCAAATTAAGAAATTGAAGGGTTGGATTCAGTCCAGAGTTCCAA
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                                                                  ATGTAGTTAATCTCTTCCTTCGTCGCGATCGCAGCTTATATCTGGACCGGCATCGCCA
                                                                                                                                                                   AATCATTCACAGCAGATGAAGAC - - - CAAGACAACGAGGATGCATTTTTCTTGATTCCGG
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Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
Gentiana triflora
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Gentiana triflora mRNA
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FPNRGIAVALTAHHSIADAKSFVWFINAWAYINKFGKDADLLSANLLPSFDRSIIKDL
YGLEETFWNEMQDVLEWFSRFGSKPPRFNKYRATYVLSLAETQKLKRKVLNLRGSEPT
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GDSITLIVAESDQDFDYLKGHQLVDSNDLHGLFYVMPRVIRTMQDYKVIPLVAVQVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCATGCTTCAGCTTCTCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACC 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGA---TCATCCGCATTCC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACTTAAA 368
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                                                                                                              cDNA cloning, gene expression and subcellular localization of anthocyanin 5-aromatic acyltransferase from Gentiana triflora Plant J. 16 (4), 421-431 (1998)
(E-mail:Hiroyuki_Fujiwara@suntory.co.jp, Tel:+81-75-962-8807 Fax:+81-75-962-8262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAATCTAATCTACCCTCTATCGCCGGAGAAATGCCGGAGTTCCGGTA-----TCAG
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/protein_id="BAA7428.1"
/db_xref="GI:4185599"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                          Fujiwara,H., Tanaka,Y., Yonekura-Sakakibara,K.,
Fukuchi-Mizutani,M., Nakao,M., Fukui,Y., Yamaguchi,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1679;
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Pred. No. 1.1e-29;
                                                                                                                                                                                                                            /organism="Gentiana triflora"
/db_xref="taxon:55190"
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350 c 359 g 48:
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6. .1415
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                                                              AUTHORS
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FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCATGCTTCAGCTTCTCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 TGCAATCTAATCTACCCTCTNTCGCCGGAGAAATGCCGGAGTTCCGGTA----TCAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAATTTGTTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGAT 308
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                                                                                                                     PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 GTTATCCCTAATCTTAAGGCCTCTTGTCTCTCAAAACACTACGTTCGCTTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor'
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY PALENL: JP 1997070290-A 1 18-MAR-1997; SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 193; DB 10; Length 17
Pred. No. 1.1e-29;
0; Mismatches 605; Indels

    .1703
    /organism='Gentianatriflora'
    /vartety='japonica'
    /tissue_type='petal'
    /clone='pGAT4'

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/organism="unidentified"
/db_xref="taxon:32644"
. 350 c 359 g 48;
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strandedness: Double;
topology: Linear;
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                                                             Gentianatriflora
JP 1997070290-A/1
18-MAR-1997
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Best Local Similarity 51.2%;
Matches 684; Conservative
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       GGCCTAGAGGAACATTTTGGAACGAAATGCAAGATGTTCTTGAAATGTTCTCTAGATTT
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                                                               TTGGACGGAAAAGGTGAATGTTTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCT
                                                                                                  TTGTCCGCGA-----ATCTTCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTAT
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1 (bases 1 to 1703)
Ashikari T., Tanaka, Y., Fujiwara, H., Nakao, M., Fukui, Y.,
Yonekura, K., Mizutani, M. and Kusumi, T.
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ON E12753.1 GI:3251585
JP 1997070290-A/1.
unidentifled.
Munidentifled
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REFERENCE AUTHORS

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Patent: JP 1997070290-A 5 18-MAR-1997;
SUNTORY LTD
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293 c 296 g
                                                             30-JAN-1996 JP 1996046534
17-FEB-1995 JP 95P 6713
                                                                                                                                  C12R1:865),
PC (C12N9/10,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key Location
FT source 1..1508
FT //tissue_
FT CDS 1.1367
FT CDS 1.1367
FT CDS 1.1367
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                                      GGCCTAGAGGAAACATTTTGGAACGAAATGCAAGATGTTCTTGAAATGTTCTCTAGATTT
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                          TTGGACGGAAAAGGTGAATGTTTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCT
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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   196915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGCCATCGCTCGTTA 62
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 TCGCCGG-------AGAAAATGCCGGAGTTCCGGTATCAGAACGGTGACTCG
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/clone='pCAT48'
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    1508
    /organism="unidentified"
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JP 1997070290-A/2.
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                                           REFERENCE
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AAAGGCTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTT-----AACGAAA
                                                                                    TTGAGACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTGAT
                                                                                                                      114 AAAGTTCGGTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAAAGAAAAAGGTC
                                                                                                                                                     CAGAGAAAAGCCCCAAATGTAGTTAATCTCTTCCTTCGTCGCGGTCGCAGCTTATATC
                                                                                                                                                                           774 TTAACCCAAGTGCCAAACTTGGAGTACATGTCATTTTACGGTAACTTGTGGTTATATA
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                     GAATGTTTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCTAAATTGGACACATAT
                                         GGATCTCCACCGGTTTTTGATAGATTGATT - - - AACATCCCACATTAGATGAAATAAG
                                                              AAATGAAAAA 1489
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24 -JUN-1998

E12754 1622 bp DNA PAT 24-JU Gentianatriflora mRNA for acyltransferase, complete cds. E12754 GI:3251586

LOCUS DEFINITION ACCESSION VERSION

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PI FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
C12R1:865),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 GTAGATTCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTA 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 ACGATTATGGAGTCTGTCGGAGATCATCCGCATTCCGCTCATAAATACTACTGCTTTGCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 TTGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                 PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 TTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAA
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                                                                Nakao, M., Fukui, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1622;
                                                                                                        ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism='Gentiana triflora'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 153.8; DB 10; Length
Pred. No. 1.2e-21;
0; Mismatches 652; Indels
                                                         Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROFIBIN HAVING ACYL GROUP TRANSFER
PETENT: JP 19970;0290-A 2 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35. .1474
/product='acyltransferase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type='petal'
/clone='pGAT106'
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/organism="unidentified"
/db_xref="taxon:32644"
1 345 c 322 g 47:
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topology: Linear;
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                                                                                                                                                                   Gentianatrifilora
JP 1997070290-A/2
18-MAR-1997
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Best Local Similarity 49.4%;
Matches 692; Conservative (
                                            (bases 1 to 1522)
unidentified
unclassified.
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                                                                                                                      GTTTTGGTTGACAAATCCAATGGAGATTC---ATTAAAGTTCCTTCCACTTTCTTCTTA 649
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GCTTCCATCACTAAATTCGGAGGAGATGATGAATTCTTGGACGGAAAAGGTGAATGTTTG
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                                        ATAACGACGCACCACCACCGTTAGCGATGCTCCATCGTTTGTAGGGTTTATGAAGAGTTGG
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AB026494 1622 bp mRNA PLN 04-APR-2000 Gentiana triflora GAT106 mRNA for acyltransferase homolog, complete cds.

LOCUS DEFINITION

RESULT AB026494

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HLHFYRERHPCPUSKFTISSIKSSLSIVLKHFLDLAGNLIMPDSSDRWPELBYKKGD
SVSLTIAESSMDFDYLAGDHQRDSYKFNDLIPQLPEPIVTSGDEVLPLFALQVTVFSN
TGCICGRALHGYLGABASSFHNKLWAVLDKRGRDSLKFLENSLPWRDSRVQDPFH
IRKTYNERKLIKSGGTPTVLNPAISKDEVBATFILHPIDIMKLKRISSRYNLIGS
SNYNLSTFTVTSALIWTCLSKSLDTVVREKVBEDKHANLCAFINCRQRFAPPIPQN
FGNCIYPCMGSTHEQLYGRELSVAATAIGDAIHRRLHDYEGILRGDWISPPRSTSA
APRSTLIYVGSAQRNVHDFDBADFGWGKLEKHESVSTNPSATLILISRSRRFKGALEL
GISLDRNRMDAFFTTNFIISTNFINGRUKLEKHESVSTNPSATLILISRSRRFKGALEL
345 c 322 9 477 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frutescens and diverse plant acyltransferase homologs
Unpublished (1999)
2 (bases I to 162)
3 (bases I to 162)
4 (bases I to 162)
5 (bases I to 162)
5 (bases I to 162)
5 (bases I to 162)
6 (bases I to 162)
6 (bases I to 162)
7 (bases I to 162)
7 (bases I to 162)
8 (bases I to 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MAGNSEDIKVLEKCRVAPPPDAVAEFTVPLSFFDMRWLISDAEH
                                                                                                                                                                                 Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                     Yonekura-Sakakibara, K., Tanaka, Y., Fukuchi-Mizutani, M., Fujiwara, H., Fukui, Y., Toshihiko, A., Yamaguchi, M. and Kusumi, T. Molecular clonding and blochemical characteization of hydroxycinnmamoyl-CoA:anthocyanin 3-0-glucoside-6-0-hydroxycinnamoyltransferase from Perilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CICCCGCTCACCTICTTCGACATGACGTGGCTGCATTTCCACCCCATGCTTCAGCTTCTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Gentianaceae; Gentiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ACCACCTCCTCGAATCCTCCCGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAA
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49.4%; Pred. No. 1.2e-21;
Live 0; Mismatches 652; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homolog

    1622
/organism="Gentiana triflora"
/db_xref="taxon:55190"

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/protein_id="BAA93452.1"
/db_xref="G1:7415597"
                                                                   acyltransferase homolog.
Gentiana triflora cDNA to mRNA.
Gentiana triflora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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35. .1474
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/gene="GAT106"
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hes 692;
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ORIGIN
                                                                                                                                           ORGANISM
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REFERENCE
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ACCESSION
                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                          REFERENCE
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The software programs used to predict genes include: Grail tinformatics Group, Oak Ridge National Laboratory, http://compbio.orni.gov/Grail-1.3/, GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Heksgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zcol.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan.SE (Sean Eddy, Washington University, School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan.SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5′ clone is K1556 and the 3′ clone is X3X3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (18-AUG-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/Kaoso/cgi-bin/agd_graph.cgi?c=mxFl2
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'
protein similarity are described as 'unknown protein'
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pddvyatsrsmgnadhpequlnfutwlftvdagfsylvrlhfcetlsevnkegqrvf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Braßsicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Sato,S., Kaneko,T., Nakamura,Y., Kotani,H., Miyajima,N.
                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thallana (strain:Columbia) DNA, clone_lib:Mitsui Pl
clone:MXF12.
                                                                                                                                                ABU16892 66237 bp DNA PLN 27-DEC-2000 Arabidopsis thallana genomic DNA, chromosome 5, Pl clone:MXF12. AB016892 BA000015 AB016892.1 GI:3449127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural analysis of Arabidopsis thallana chromosome 5. VI Sequence features of the regions of 1,081,958 bp covered by Seventeen physically assigned PI and TAC clones 99156233
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2613. .5234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3702"
/chromosome="5"
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/clone="MXF12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thallana
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/translation="mgnkklltggsskthgsgssyrdpllqnqbbkpkangsenglnd
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                                                                                                                                                                                                                        ARLRKDLFRHLMHQEIAFYDVTKTGELLSRLSEDTQIIKNAATTNLSEALRNVTTALI
GVGFWETSSKKLTLLALVVPVPISVAVKYGFGRTLRELSHTAPAAAVARSIAEBSFGA
GVGFRAERSYKLTJALVAVPISVAVKYGFGRTARELSHTASIABSFGA
YLTIKGSMTVGALTSFILXSLTVGSSVSSLKSLTTAMKAAGASRRVFQILDRVSSKA
                                                                                                                                                                                                                                                                                                                                                                 SSGDKCPVGNPDGDVELNDVWFAYPSRPSHMILKGISLRLTPGSKVALVGPSGGGKTT
TANLIERFYDPLKGKILLNOVSLMEISPGYLLHGOSISVSQBPTLENCSVEBNIAYGFD
GEASFTDIENDAKMANAHEFIEAFDKYNTVVGERGIRLSGGGKQRTAIARALLTNPS
VLLLDEATSALDAESEYLVQDAMDSLMAGRTVLVIAHRLSTVKTADCVAVISDGEVAE
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LNAWHRVAKVFTGGKEPENPKSLKLLMSPEIGPDVFRYTLNLTREDIQKLRERLKKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence-not_experimental
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SFSVAETNADFSSLSGNEPFPSTELXPLVPALQSSDDSASIVSFQVTLFPNQGFCIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAHHAVLDGKTTTMFLKSWAHICKHODFSLPQDLIPTVDRTVIKSPTDSENKVLNEWR
SFTKILAGGKEPANPKSLKLNPSFEIGPDVVRYTLQLTREDIOTLRERLKREVSSSS
STSSSKELRLSTFVIVYSYVLVCIIRARGGEPHRPVGYAFSVDCRSLMNPPTPNYFGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYFETFMSEEGFLAAARMVSDSVEALDENVALKIPEILEGFTTLSPGTQVLSVAGSTR
FGVYGLDFGWGRPEKVVVVSIDQGEAISFAESRDGSGGVELGFSLKKHEMDVLVDLLH
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TLYGSSNREGVYELDFGWGRPDKVMVVSISPGNGISMAESRDQNGSVELGFSLKKHEM
DTLIDLLHCELTI"
34363. 35709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSSSVSSSPKELRLSTFVIVYSYALTCLIKARGGDPSRPVGYGFAVDCRSLMVPPVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 CCCCATGCTTCAGCTTCTCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAAC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 CACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCTTCGACATGACGTGGCTGCATTTCCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
product="anthocyanin acyltransferase-like protein"
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/db_xref="G1:10177550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprement(join(30804. 30874,30947. 31289))
/hote="contains similarity to Ac-like transposase gene_id:MXF12.9"
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Pred. No. 9.9e-12;
); Mismatches 716; Indels
/product="ABC transporter-like protein"
/protein_id="BAB10828.1"
/db_xref="G1:10177549"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGTHDELLSLNGIYTNLVKRQLQSSSSVTTL"
join(25348. 26359,26401. 26756)
/note="gene_id:MXF12.7"
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complement(join(30804. .308
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/evidence=not_experimental
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Best Local Simi
Matches 664;
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LRLYFYPTQYKSGFDAVNSFFSVKVNGFTLLRNFNADSTVQASIPLSNSLIKEFIIPV
HQTLNITFTPSKNLLAFVNGFEIVSMPDRFYSRGGFDNVLRNSSDVDFQIDNSTAFE
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VXATSRLMGNSSNLMFNLTGMFLTTVDAGYNITVRTHFCFTLPQVTKAQORVFSTFVD
KMAKKETDVIRLSGGPRIPMYLDFSVYVGFESGMIQPELRLDLVPLKDTNQTYYDAIL
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WTQEEKNILERNSDNASFSSVVSYKEESGIPQVPYMTARIFRSDFTYSFPVSPGWKFL
RLYFYPTSYKGSFDANNSFVSYTVNDFTLLQMFSADLTVKASTBERSKELIKEFYPVY
UFLNLFFFRSNNSLAFVNGIELVSMDRFYSKGGFDDLITNVGSLIDFEIDNSTASET
VYRLNYGGHWYDDFYNDSGMFRWLSDDYSFLIGGVSPYMDDVNISYTEKTPAYVAPAY
VYSTCRMMGNAQDTYLNLWFNLTWLFTVDAGFSYLVRLHFFEKYLNKANQRVFSIFLG
                                                                                                                                                                                                                        VVKGTFGYLDPEYYRRQVLTEKSDVYSFGVVLLEVLCCRPIRMOSVPPEQADLIRWYK
SNYRRGTVDQIIDSDLSADITSTSLEKFCEIAVRCVQDRGMERPPMNDVVWALEFALQ
LHETAKKKNDNVESLDLMPSGEVGTTTDGEDDLFSRTTGHVGKSTTTDDSVLVVGDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MINLEKEAKEKQILIRDGKRKIVHHVNTTLLVKIYEASAIDDRH
LFLKPYYGPPNYYFIKAWLDDTKEYGTYVVKDSFKVNQPPLKIPLNFPAQYLYVELLK
GMSYRDPGTSNRTVVMGRAKIRLSPLMTSYKERPISGGIDLVGLNSDQCVVKKGYLTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGVEILKLNDSDGNLARPNPELLVSTDSTPDDSNVTPPIKGKPHVLVIILIVVGSVIG
LATFIVIIMLLIRQMKRKKNKKENSVIMFKLLLKQXIYAELKKITKSFSHTVGKGGFG
TVYRGNLSNGRTVAVKVLKDLKGNGDDFINEVTSMSQTSHVNIVSLLGFCYEGSKRAI
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NGVEILKLNNSGNLAIJQDNELKPNPPLSSNLTPNHVTQQIKGKSSHLLVKIFIAVGP
GTGLATFVVVLMLWMRQMKRKNRKEERVVMFKKLLNMYTYAELKKITKSFSYIIGKGG
                                                                                                                                                       LSKLRHVHLVSLIGYCDEDNEMVLVYEYMPHGTLKDHLFRRDKTSDPPLSWKRRLEIC
IGAARGLQYLHTGAKYTIIHRDIKTTNILLDENFVTKVSDFGLSRVGPTSASQTHVST
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ILLDDNFCPKVADFGLAKLCEKRESILSLIDTRGTIGYIAPEVVSRMYGGISHKSDVY
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KMILVSLWCIRPCPSDRPPMNKVVEMIEGSLDALELPPKPSRHISTELVLESSSLSDG
QEAEKQTQTLDSTII"
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AIVYEFLENGSLDQFMSRNKSLTQDVTTLYGIALGIARGLEYLHYGCKTRIVHFDIKP
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VYSFGMLVIDMIGARSKEIVETVDSAASSTYFPDWIYKDLEDGEQTWIFGDEITKEEK
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                                                                                   SLVVLAMFVVGVLVIMKKKKKKKSKPSTNSSWCPLPHGTDSTNTKPAKSLPADLCRRFSI
                                                                                                                          FEIKSATNDFEDKLIIGVGGFGSVYKGQIDGGATLVAVKRLEITSNQGAKEFETELEM
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17337. 17461,17541. 17640,17803. 17944,18073. 18191,
18285. 18395,18488. 118632,18712. 18844,18934. 19009,
19232. 19297,19385. 19492,19591. 19698,19873. 20070,
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/product_rereptor protein kinase-like protein"
/protein.id="BAB10827.1"
/db_xref="GI:10177548"
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/protein_id="BAB10826.1"
/db_xref="GI:10177547"
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/note="gene_id:MXF12.5"
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                                                                                                                                                                                                                                                                                                                                 SGSSWGVFSEINEPKAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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_	1230 AGAGAAGTTTACGATGTCGTTGTAAACCGAGGATGCTGCCGGAGGATTGGAGGTTGG 1289	0y 1230	0
RE	1170 TTACGCCCCGATTTTGGATGGGGTAAGGCCGTGAAGCAAGTACTGTCGATTGATGG 1229 	QY 1170 Db 35529	<u>σ</u> Δ
			Ω
	GATTCGCGAAGCCTTGCAAAACTGTTATTTCTCGGTGGCGGGATCGAGCAGGCTTGATCT 1169	Oy 1110	0
	1050 AATAGAGAAGAGGAGGAGCACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGA 1109 110	Oy 1050 Db 35409	0 0
RE	35349 AGATGCGGCGATGTTTCTTGGTGAACAAGGTTTCGTGGTTGCTGCGGGCGATTGATT		ν Ω
	TCCACCGATCCCGTTGACTTATTTCGGAAACTGTGTTTACTCTGCTGTGAAAATCCCGGT 35348 GCGGCGGATTTGGTCGGAAGAAGGGGTGTTTTCGGCAGCTGAAGGGAATCGGGAGA 1049	DD 35289	o c
	TCCGCCGCTCCGGGGAACTACTCGGAAACTGTCTATCGTTTGCGATGCCGAAGATCCT 989		0 6
	GGATGACGACAAACGCGCTTTCTTTTAATTCCGATCGATTTAAGGCCGCGTTGGA 929	Oy 873 Db 35229	0 0
	GCAGCTTATATCTGGACCGGCATCGCCAAATCGGTCGGAGATTACAAAGACGT 872 	Oy 820 Db 35169	0 0
	AAGGGTTGATTCAGAGAAAAGCCCCAAATGTAGTTAATCTCTTCTTCGTCGCGATC 819	Oy 760 Db 35109	0 0
	ACCGACGGATCGGATTCGAGCTACCTACCTTTCACCCAATCTGAAATTAAGAAATTG 759 	Oy 702 Db 35049	0 0
	GGACACATATTTATGGAACAACGCGCAGAAACGTCCGTTGGAATCGCAGCATCCATC	Oy 642 Db 34989	0 0
33.	CGGAAAGGTGAATGTTTGCCGGTTTTGGACCGATCGCTCGTGAATTATCCGCCTAAATT 641 	Oy 582 Db 34929	0 0
2 S	AGGGTTTATGAAGAGTTGGGCTTCCATCACTAAATTCGGAGGAGATGATGATTCTTGGA 581	Oy 522 Db 34881	0 0
	TCGCGGGGTGTGCATCGGAATAACGACGCACCACCGTTAGCGATGCTCCATCGTTTGT 521 	Oy 462 Db 34821	0 0
B & C 2 5	CGAGGAATCTGATCGGAAATTGTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGG 461 	Oy 402 Db 34776	o ä
 	TAMATACTACTGCTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCGATAGT 401	Oy 342 Db 34716	0 0
	CGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGATCATCCGCATTCCGCTCA 341	Oy 282 Db 34656	0 0
à à	TTCATGCAATCTAATCTACCCTCTATGGCGGGGAAAATGCCGGAGTTCCGGTATCAGAA 281	Qy 222 Db 34599	O D
<u> </u>	CGTCGTTCCGAAACTCAAACATCCTTATCTCTAACCCTCAAACACTTCTT	Oy 165 Db 34539	0 0

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United (26-7AM-1998) Arabidopsis thaliana Genome Center, Submitted (26-7AM-1998) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (Dases 1 to 101176)

S (bases 1 to 101176)

S (cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Chio, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lerz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, P., Sakano, H., Schwartz, J., Southwick, A., Thaveria, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Pederspiel, N., Theologis, A. and Ecker, J.

Direct Submission

L Submitted (28-UNW-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA

E (bases 1 to 101176)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC002560 101176 bp DNA PLN 19-JUL-2000
Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 101176)
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Direct Submission

Submitted (13-NOV-1997) Arabidopsis thaliana Genome Center,

Bepartment of Biology, University of Pennsylvania, 38th Street and

Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

Ecker J.R.

Direct Submission
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35646 CTTCTCGCTCAAGAAACA, GAAATGATGTTTTGATTGATTTGCTACACAGGGGATAAA 35705
                                                                                                                                                                                                                                                 35706 ATGATAATGGAACAAAAT!!AAGATTTAATTCAGTGTGTCTCTCTTGTTAGCTTGCATCGA 35765
                                                                                                                                                                                             1350 GGGTTGATTAATCATTTAAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTC 1409
                                                                                   1290 ATTGTCTTTGCCAAAGGAGGAATTGCAAGCTTTTGATGATTATTTTGCGGAGGGAATAAA
                                                                                                                                                                                                                                                                                                                                    1410 TATTGTTTAAACAATAATATTTTCCATTGAACTTTTTTGAGTCAATA 1457
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Ecker, J.R.
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AC002560
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JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT FEATURES

CDS

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join(11965. 12015,12038).12173. 12303,12448. 12519,12596. 12685,
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SERISMPCFVSTFMKRNPRITYDIRELLERDDMAKTRDLITTERSWTRITE
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VEVLERMIQGIRGFHEQEPEAKKRFYSRDHTRDVLYFSNHDLQNSEAASWRDTLGCYT
                                                                                                                                                                                                                                                                                                                      APEPPRLEDLPAVCGEIMLEYSKEIMSLGERLFELLSEALGLNSHHLKDMDCAKSQYM
VOGHYPROPODLTTGINKHTDISFLYLLQDNYGGLQYFERDYWIDYPVPGALVIN
IGDFLQVKITMLLLESCFISCHINGIILLEYCVQLITNDKFISAEHRYLANGSSEPRT
SVAIVFSTFMRAYSRVYGPIKDLLSAENPAKYRDCTLTEFSTIFSSKTLDAPKLHFFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mntivvaoloropody ivslyogoflungfselrklodegtpdf
vaevvslefeddcsklintmsislerpdnvdfkqvdsgvydkgsssslcfvlsvgarr
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nvsfklcenllylllekqilqagqtipqvdin"
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IQPANQVTISTVDLSYNRFSGGISPLLSSVENLYLNSNRFTGEVPASFVERLLSANIQ
TLYLQHNFLTGIQISPAAEIPVSSSLCLQXNCMVPPLQTPCPLKAGPQKTRPTTQCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(18462. .18515,18612. .18742,18840. .18975, 19064. .19139,19214. .19410,19497. .19595,19668. .19752, 19865. .20103,20179. .20253,20345. .20649,20798. .20902, 21088. .21216,21356. .21437,21513. .21668,21780. .21849, 21929. .22025,224408. .22502,22586. .22569,22880. .23041. .23101,23206. .23315,23411. .23556))
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GGETPSPYKGHYMDIAAQRWLVIFSGNNGNBILIDDTWALDTRGPFSWNDRLNPSGNNPS
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SMDLISRRSVVEKIGDAAERWGFFQVVNHGISVEVMERMKEGIRRFHEQDPEVKKRFY
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ISPSIGSLPELSNLILCHNHLTGSIPPFLSQTUTRIDLKRNSLTGSISASLPPSLQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16495. .17682
/note="similar to protein kinase pir||A57676; similar t
ESTs gp|A1993651.1, dbj|AV538995.1, dbj|AV522524.1, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10833. .11348
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L. Submitted (19-JUL-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
On Jul 15, 2000 this sequence version replaced gi:2618677.

Location/Qualifiers
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PEPFGERGOTLMYSANSSMDLADLGDTVPNPAMPLIFIRMGERAVKILEMPLIAO
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FEMYETADFGWGKPVYAGPIDLRPTPQVVCVLLPQGGVESGNDCSMVCLCLPPTAVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANGWMEKPVTAKLSTLKETRITNGFTTPPILTDSVNEQMLSTGKPPMGFGFALHEEHC
KAVADPKEEHLKKKLDEVTNVHHLNVNNNTEKLQGDKMVNSQVLNAFGVCILYKDFL
                             Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104–6018, USA 7 (bases 1 to 101176) Cheuk,R., Shinn,P., Brooks,S., Buehler,E., Chao,Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(736. 1038,1276. 1713,1874. 2119,2205. 3032, 317. 3274,3483. 3610,3725. 4134,4313. 4435) //notea-unknown protedin; similar to ESTS dbj|AV529515.1, dbj|AV522866.1, dbj|AV54950.1, dbj|AV523761.1, dbj|AV523761.1, and dbj|AV523761.1, and dbj|AV546743.1"
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Submitted (15-JUL-2000) Arabidopsis thaliana Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental/product="F21B7.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38228 ACATACTTTGGCAACTGTATGGCTCCTGGTATCGTATCAGTCAAGAAACACGATTTGCTA 38287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1006 GGAGATGAAGGGGTGTTTCGGCCAGCTGAGGCGATCGCGGCGGAAATAGAGAAGAGGACG 1065
                                                                                                                                                                                                                   TACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                        357
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                                     Gaps
                                                                     7 ACCCTCCTCGAATCCTCCCGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTC 66
                                                                                                                                                                TCCTTATCTCTAACCCTCAAACACTTCTTCCCCCTTTCATGCAATCTAATCTACCCTCTA
                                                                                                                                                                                                                                                                                                                         37451 TCCCTCTCCATCACTCTCCAACATTTCTTCCCTTACGCCGGTAAACTGATTATCCCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37748 GGCAACTCAGCTACACATGTTGTAGCAGATGGAGTCACCTTCAGTTTCATGAAGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37808 TGGATGTCATTGACCAAATCCAGCGCCAAAGATCCGGCCACGGTTCTTCTACCCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37928 GAGCGGTTTTGGAGCCAAAACTCTGCAAAACACACATCACATGTTACGCCTGAGAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37988 GTCAGAGCCACTTTTACATTGAGCCGGAAGCAGATAGACAATCTCAAGAGTTGGGTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38048 GAGCAGTCTGAGAATCAATCTCCTGTTTCTACCTTCGTGGTGACTCTAGCTTTCATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38168 CACTTCATGATCAACGTGGATTGCAGGAATCGTCTCAAGTACCACAACCAATACCACAA
                                                                                                                                             CCGCTCACCTTCTTCGACATGACGTGCTGCATTTCCACCCCATGCTTCAGCTTCTTCT
                                                                                                                                                                                                                                                                                                                                                             37571 GCAGAGTCTACTGAAACCGACTTCGACCAACTGAAGTCTGATTCCCCTAAAGATATCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGGTGTGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       598 TTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCTAAATTGGACACATATTTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37868 CCTATTCACAGCTGCAGAAACATAATCAAGGACCCAGGAGGTAGCCGCAGGACATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C---GAGCTACCTATCTTCACCCAATCTGAAATTAAGAAATTGAAGGGTTTGATTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               775 AGAAAAGCCCCAAATGTAGTTAATCTCTTCCTTCGTCGCGATCGCAGCTTATATCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCGGCATCGCCAAATCGGTCGGAGATTACA---AAGACGTGGATGACGACAAACGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAAGCTTGATTAAGACACTTGTTCAAGACAGTGAAACAGAGGCCAAGGACGAAGTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCGATAGTCGAGGAATCTGATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 GGAATAACGACGCACCACACGGTTAGCGATGCTCCATCGTTGTAGGGTTTATGAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 TGGGCTTCCATCACTAAATTCGGAGGAGATGATGATTCTTGGACGGAAAAGGTGAATGT
Length 101176
                                     27;
                            0; Mismatches 718; Indels
DB 12;
                    .5e-11
Score 102.2;
Pred. No. 7.5
                  Pred. No.
6.7%;
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 Query Match
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Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Yu, G., Osborne, B. L., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
Direct Submission
Submitted (12-007-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo Alto, Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, F., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskalar, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskala, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Submission Submitted (30-JAN-1999) DNA Sequencing and Technology Center, stanford University, 855 California Avenue, Palo Alto, CA 94304, Federspiel, N.A., Pain, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskala, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. 18288 GGAGAAAAATGCGTCATGGCTGCTTCAGATGCAATCACAGGGAGAATCAAAGATATTA 38347 38467 CA 94304, USA
3 (bases 1 to 119314)
Federspiel,N.A., Palm.C.J., Conway,A.B., Conn,L., Hansen,N.F.,
Altafi,H., Araujo,A., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.,
Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W. Submitted (30-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, PLN 30-JAN-1999 I BAC F21M11 genomic sequence, GGATGGGGTAAGGCGGTGNAGCAAGAGATACTGTCGATTGATGGAGAGTTTACGATG 1246 TCGTTGTGTAAACCGAGGGATGCTGCCGGAGGATTGGAGGTTGTTTTGCCAAAG AGCGACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGAGATTCGCGAAGCCTTG TCAAGCGATCTGTTGAAGACAGCACCAAGATGGGGACAAGGAGTACGTAAATGGGTCATG CAAAACTGTTATTTCTCGGTGGCGGGATCGAGCCAGGCTTGATCTTTACGGCGCGGGTTTT 1306 GAGGAATTGCAAGCTTTTGATGATTATTTTGCGGAGGGAATAAAG 1350 chromosome DNA (bases 1 to 119914) AC003027.1 GI:4079614 AC003027 119914 bp Arabidopsis thaliana complete sequence. 10 DEFINITION ORGANISM TITLE JOURNAL 1186 TITLE JOURNAL TITLE JOURNAL 1066 38348 REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE AUTHORS REFERENCE AUTHORS RESULT 1 AC003027 REFERENCE AUTHORS REFERENCE JOURNAL LOCUS δ g ò g δ q ò qq õ g

COMMENT

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/ POTOTE 11_16="G1:4204288"

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FESETDANHTPPESTTEQARKNVRDITASEQPSNARRRICGDSFIQESSPNRYTQDP

TLIRIMESLRSDDPTDY VRAONHWYDKTENNIAMGSANIECVVFCVQQLPR

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POYYT RGDTYKNLARALLARGWRIKCTYCSLKGAALGCFWSCRRSYHVPCAREISRCR

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SALSKSDKKLMESLANRENATISRYWNPSVTHVIASTDEKGACTRTLKYLMGILNGKW

INNAMMASLKASOPVDEEPFEIQIDTGCGOGGPRYRTRRRLARTINKRLFEGIKFYFF
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DSLHNPTKEVYTQDIGDKTEEIDSKLRRSNETVRDGNHYDGGGVLNPVENLTQWKSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKGRTKQKQSQKENSNFIADQEEKRDSSSFGTDPQIDDITLSYKPKCRIEPKKLRNQE
LAVDASLSTWLSTSESGSECNSASMYTLTPEKLKSTSCYSKPLRINHDDRPVLCALTL
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REDKSVNWHSTPFEARLEKALNNIDK"
complement (16835. 20238)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(16835. 17185,17274. 17392,17491. 17565, 17795. 17885,17982. 18079,18175. 1836,18504. 18604, 18705. 19049,19134. 19349,19439. 19791,19862. 19967, 20188. 20238).
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KWLDQHIHAYFAVGAPLLGSVEAIKSTLSGVTFGLPVSEGTARLLSNSFASSLWLMPF
SKNCKGDNTFWTHFSGGAAKKDKRVYHCDEEEYQSKYSGWPTNIINIEIPSTSARELA
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PRPPTKNVFCIYGAHLKTBVGYYFRDSKRYPDMNITDDITYFEGSLVSRSGTVVDG
NAGPITGDETVPYHLSJWCKNWLGPKVNITMAPQILJGKIKQDFEHDGSDVHVELNVD
HEHGSDIIANMTKAPRVKYIIFYEDSESIPGKRTAVWELDKSGY
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GEEVTIIWQRANDAEALASQTGSRLVGHTWVLESIAGYKLHPVIG"
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16327. .16362))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Hypothetical protein"
               complement(14004. .16362)
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27777. . .28734
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/gene="F21M11.5"
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                                                                                                                                                                                                                                                                   /codon_start=1
               gene
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                                                                                                                                                                        Genes with similarity to proteins in the databases are described as Genes with similarity to proteins in the databases are described similarity but no 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'nuknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (chris Burge, http://gondic.stanford.edu/-chris/GENSCANW html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
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LHFGSMCCSKSKCDGMDAWIFDIDDTLLSTIPYHKKGFFGGEKLWTKFEDWIQKK
APAVPHMKKLYHDIRERGIKIFLISSRKEYLRSATVDNLIOAGYYGWSNLMLRGLEDQ
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complement(join(14004. .14312,14565. .14641,14787. .15831,
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On Dec 30, 1998 this sequence version replaced g1:2734094.
Basses 1-9262 of clone F21MI1 overlap with bases 6898-78259 of
TARWU' BAC clone F20022 (AC002411) and bases 119525-119914 of clone F21MI1 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Proteins in this region are annotated in the F21M11 entry, AC002411."
1. .9262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AaD10665.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRRNGERGLAMTVINNASPSSSRLSMEPEEVPPMVLLPAHPMETKVSEASALVILND
EPNIDHKPVISDTGNCSAPMLEMGKSNIHVQEWDWETKDILNDTTAMDVSPSSAIGES
SEHKVAAASVELASSTSGEAKICLSFAPATGETTNLHLPSMEDLRRAMEEKCLKSYKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHPEFSVLGFMKDMCSCYIDLAKNSTSQLLETETVCDMSKAGDESGAVGISMPLVVVP
ECISGOGMRATISNMKDITAGEBNVETEPWNETNETNEVRYMPHSYFYGDAPYIFS
LSSFSDEGSCSTSCIEDCLASBANGSNKCAIGVDNGFAYTLDGLLKEEFLEARISBARDO
RKQVLRFCEECPLERAKVEILEPCKGHLKRGAIKECWFKCGCTKRCGNRVVQRCMHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLQVFFTPNGKGWGLRTLEKLPKGAFICEYIGEILTIPELYQRSFEDKPTLPVILDAH
WGSEBRLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'translation="MDRTMFLSLTIASLLVGVVSAGDWNILNQLRGLGSSSSQNGIVS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="overlap with bases 68998-78259 of 'IGF' BAC clone F21M11."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDIEAMEELAWDYGIDFNDNDSLMKPFDCLCGSRFCRNKKRSTKTMQILNKA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(7684. 7866,7965. 8027,8122. 8160,8250. 8381,8458. 8728,8875. 9893,10003. 10256,10344. 10410,10501. 10551,10685. 10781,10885. 10913)
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110C2T7 , gb[f42036, and 110C2XP, gb[A1100245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Join(13061. 13488,13717. 13926,14139. 14316)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .119914
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Hypothetical protein"
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/gene="F21M11.1"
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/translation-"MNTKTMRLPPRRVLTADKRKERDAFISSVTDNPPEIAKFPSPPP
KLVPPPVNPISKKSSTAAAEPIGSNQLMLAGYLSHEYLTQGTLFGGQWNQARAQAESS
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                                                                                             /gene="F21M11.7"
complement(join(29264. .31015,31312. .31414,31484. .31587,
31782. .32033)
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                                                                                                                                                                                           Length 119914;
                                                                                                                                                                                      Score 87.8; DB 12;
Pred. No. 7e-08;
0; Mismatches 717;
                                                                     complement(29264. .32033)
                                                                                                                                                                                         5.8%;
|larity 44.9%;
|Conservative
                                                                                                                                                                                                               Best Local Similarity
Matches 617; Conserv
                                                                                                                                                                                         Query Match
Best Local 9
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Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thallana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC and BAC clones
DNA Res. 7 (3), 217-221 (2000)
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Sukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyJedons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
47210
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Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:MODL
AB028618 BA000014
                                                                                                                                                                                                                                                                        ATTTGGTCGGAGATGAAGGGGTGTTTCGGGCAGCTGAGGCGATCGCGGCGGAAATAGAGA
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                                                                                                                    CTCCGGGGAACTACTTCGGAAACTGTCTATCGTTTGCGATGGCGAAGATCCTGCGGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence-not_experimental
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//db_xref="GI:11994481"
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VOAPAKKAVKVOAPAKKVPAEGSGSTGTTATAMATNAAPTTAAPTTAPTTAPTT
ESPMINDSTFYDALKHIPAEIGENWOTDEVEDEETETNKEIACANPVEESAGDDGI
TVIEEEEERSSESDEDVNVEKSVEDEGHEDERDBDVIVEKSGEERTIDEDIANVDMEE
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TYLPSGYTHKLMRMMLEFRASIERKEWWEVONOYPIRCOIREHALISGENCKAY
PASYQSAGNMNFARTYFKTGVIRREDVKTKLMEMEPASKDRLRMAALYFLTSIIVMP
TKTGERASPIDDFCVRSASDLTFCKIFPSGRYSFEYMLKSISHKLDHFNGVVPNTQSP
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HVLGTTEVIESIIREKAEEVPLLAEITGVEDDVDKHDVVVDSWMKRLGQGREIRFEEV
YNEDVQARWEAPNEEEVPTAVGPGDPTLVDVMEKLHSINDKLNEALLVLMEIEEKQAT
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PKLFQLLPYLSKEKVNARNLMLPPAKENINVVRVTLELSEANIKKLKEQAKNESTWSD
LLLSTFVVTYEKSSGQSLFCKEEAKKSL"
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Klsessshdsffstipklegslslaltnfipelsghikwdpodpkphviifpodtvs
Klsessshdsffstilpklegslslaltnfipelsghikwdpodpkphviifpodtvs
VGTIPOGFVLPTHSDFTVINVSVGLEFFSIGLTTHVINDGKTSTNFHKSWAHICK
YGTIPOGFVLPTHSDFTVINVSVGLEFKILQLLSYLSGDVDNDTFTLKSPSAKEIDD
LVRYTLOLSOENIKKERFKNESTRSDLYLSFFVVKXAYVLTCVYKARGGNVDRPIR
FMYAADFRNRLDPPVPLTYFGNCVLPIDIHFGRRWVCEWRGDSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(33460. .33573,33657. .34016,34094. .34255,
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complement(36608. .37000)
//note="gene_id:MOD1.9
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(40204. .40603,40656. .40872))
/note="gb!AAC97247.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strong similarity to unknown protein" /codon_start=1
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join(32547. .32726,32904. .33122)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEMQKELKAHRAEIVNVSKVLFRNPMAPKK"
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similar to unknown protein"
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unknown protein"
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. .31674
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                          (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5 clone is T1310 and the 3 clone is T26G12.

Location/Qualifiers
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VAAHHAVLDGKTSSTFIKAWAQICKQELQSWPENLTFSYDRSLIKYPTYLDEKMIELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSLKEDQTNIRSLTSLPSSKLGDDVVLATLVLSRADIERLREQVKNVSPSLHLSTFVI
AYAWHCFVYKARGGIKDRSYSLLFVGDFRDRLDDFLDGTTFGCMIPUGCTNRRADE
FWERKGFVTAAEIISDLVKGLSSRKIETIADTFVEGFSFQSWSTQFGTIAGTRLGVY
EADFGWGRPVKVDIVSIDQGEAIAMAERRDGSGGVEIGMCLKKTEMDSVVSFFNNGLY
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KTESSRDSSTLENLEDGSLSLVLFLENFLDRGHLKWNPODKPHIYLPTFPYDSLT
VVESEADFSYISKSELLETFELLETFLSLGSLSLGITFPNQFFSIGTTVH
HVVWDGKTASKFHKSWAHICKHGTTPQDFDLPTVLDFTVVINVPAGLEQKIFQLSSYIS
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PYPLTYFGKOVLPLDFNGYEATTFKGEDGFVNGVEILSDSYKGLGSRSLESYWEVYE
EGTRNMKGTKVLTYTGSNFGIYGADFGWGRPVNTDVMSLYKNNSFSMSARRDEIGV
SLKRCEMIVFLSLFSNGFDN"
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AVOTTCWKRSGGGDANRPVRDNAADENRLDDPSPYLTYERONVLLPIDFNGYKATTEL
GKOGYVNGYEILSDSVNGLGSRNIESIMEVYEDGTKNMKLDYONYTYGSNOFGIYGS
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                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mitsul Pl"
2123. 8637
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acyltransferase/benzoyltransferase-like protein"
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                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                        /strain="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(18639.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene_id:MOD1.1"
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gene_id:MOD1.2
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                                                                                                                                                                                                                       1. .85690
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Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 136047)

Lin, X., Raul, S., Town, C.D., Benito, M., Creasy, T.H., Ronning, C.M., Koo, H., Fujil, C.Y., Utterback, T., Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M., Arabidopsis thaliana 'IGF' BAC' 'F7F7' genomic sequence near marker
                                                                                                                                                                                                                     Town, C. D. and Raul, S.
Wedical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
On Jan 19, 2001 this sequence version replaced gi:12280790.

* NOTE: This is a "working draft' sequence. It currently
consists of 4 configs. The true order of the pieces

* is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1090 GTGGAGAACTGGCCGTCTGAGATTCGCG----AAGCCTTGCAAAACTGTTATTCTCGGTG 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 970 TTTGCGATGGCGAAGATCCTGCGGGGGATTTGGTCGGAGATGAAGGGGTGTTTCGGGCA 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1030 GCTGAGGCGATCGCGGCGGAAATAGAGAAGAGGACGAGGACAAGAAGATTCTAGAAACT 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910 GATTTAAGGCCGCGTTTGGATCCGCCGGCTCCGGGGAACTACTTCGGAAACTGTCTATCG 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91012 CCGGTGGGCTGTTATAACCGTAAGGCGGCGGAGTTTATGGAAGAAGGGATTTGTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1207 CAAGAGATACTGTCGATTGATGGAGAGAGTTTACGATGTCGTTGTGTAAACCGAGGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
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Location/Qualifiers
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0; Mismatches 287; Indels
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46028 a 22872 c 22213 g 44783 t
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JOURNAL
                                             REFERENCE
                                                                        AUTHORS
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16468 TCTTTTTTCAACAATGGTTTACATAGCTAAACTCTTGTTTTGTAAGATTTTAATAATAAG 16527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         910 GATTTAAGGCCGCGTTTGGATCCGCCGGCTCCGGGGAACTACTTCGGAAACTGTCTATCG 969
comptement(46109. .47990)
/note="contains similarity to reverse transcriptase
gene_id:MoD1.13"
                                                                                                                                               /evidence-not_experimental
comptement(j0in(48707. .49066,49148. .49372,49477.
49850. .49982,50772. .51282))
/note-"gblAAF06088.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 85690;
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Arabidopsis thallana chromosome I clone IGF-F7F7,
PROGRESS ***, 4 unordered pieces.
AC069470.10 GI:12320593
HTG; HTGS_PHASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                               5.1%; Score 77.8; DB 12;
llarity 48.5%; Pred. No. 7.6e-06;
Conservative 0; Mismatches 287;
                                                                                                                                                                                                                                                                             similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                      /evidence-not_experimental complement(52336. .56745)
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                                                                                                                                                                                                                                                  gene_id:MOD1.14
                                                                                              /codon_start=1
/pseudo
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Souciet, J. L., Algle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
1 (bases 1 to 1167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies(1) FEBS Lett. 487 (1), 3-12 (2000)
                        TTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAATAATTTTTTTCC 1435
                                                            Clone BAOAB017A09 of library BAOAB from strain CLIB 210 of Kluyveromyces lactis, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boldin-Fukuhara, M., Toffano-Nioche, C., Artiguenave, F., Duchateau-Nguyen, G., Lemaire, M., Marmeisse, R., Montrocher, R., Robert, C., Termier, M., Wincker, P. and Wesolowski-Louvel, M. Genomic Exploration of the Hemiascomycetous Yeasts: 11.
                                                                                                   Kluyveromyces lactis
FEBS Lett. 487 (1), 66-70 (2000)
                                                                                                                                                                                                                                                                                                                    AL427102.1 GI:12210296
STS.
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clone BA0AB017A09 of
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Patent: WO 0032789-A 40 08-JUN-2000;
AHARONI ASAPH (IL) ; VERHOEVEN HARRIE ADRIANUS (NL) ; LUECKER JOOST
JOHANNES VAN (NL)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 1648)
Aharoni,A., Verhoeven,H.A., Luecker,J., O'Connell,A.P. and Van
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YFDQNNGYSFAVABWSSECHAGFHHSGNGIRGAVBFHPLVPQLSLFDDKABVIAIQ
YTLPPNQGFGIGVSSHAILDGKTSTLFLKSNAYLCKQLQLGHPGLSPELTPLLDRT
VIKDPTGQDMLQLNKWVGSDNSDPQKIRSLKVLPFLDSESLNKLVRATFELTREDIT
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IIVGFTADYRSRLDPPIPLNYFGNCNGRHCETAKASDFVQENGVAFVAEMLSDMVKGI
DADAIEANDDKVSEILEILKEGAMIFSVAGSTQFDVYGSDFGWGRPKKVEIVSIDRTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAC09066.1"
/db_xref="G1:10187185"
/translation="MAAIENRVTLKKHEVTKVTPFVNPNSKTTSFTLDLTYFDFFWFK
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91429 GTAATGCTTGGTTATTCTTGTTTTTTTTCTCACAGAAGTATTGGGCATAATTCTCC 91488
                                       1387 GAIGAAATCCTCTGTTTCATCTCTATTGTTTAAACAATAATTTTTTTCCATTGAACTTTT 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCTCGGTGGCGGGATCGAGCCTTGATCTTTACGGCGCGCGATTTTGGATGGGGTAA 1196
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Pred. No. 0.00012;
0; Mismatches 143; Indels 12;
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Sequence 40 from Patent WO0032789.
AX025514
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/db_xref="taxon:2708"
                                                                                                                   Lemon acyl transferase"
/codon_start=1
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="part of mitochondrial DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Kluyveromyces lactis"
/strain="CLIB 210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /variety="lactis"
/db_xref="taxon:28985"
/clone="BA0AB017A09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="BA0AB"
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ο		<u></u>	U	U
Best Local Similarity 54.5%; Pred. No. 0.00018; Matches 91; Conservative 19; Mismatches 57; Indels 0; Gaps 0; 1356 ATTAATCATTTAATCATGAGTTGATGAATCCTGGTTTCATCTGTTGT 1415 1111:: :: :: :: :	RESULT 15 AP000606 LOCUS AP010606 82360 bp DNA DEFINITION Arabidopsis thallana genomic DNA, chromosome 3, Pl clone: MTO24. ACCESSION AP000606 BA000014 VERSION AP000606.1 GI:6045161 KEYWORDS ARABIGOPSIS thallana (strain:Columbia) DNA, clone_lib:Mitsui Pl clone:MTO24. ORGANISM Arabidopsis thallana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Bukaryota; Viridiplantae; Core eudicots; Rosidae; eurosids II;	Brassicales; Brassicaceae; Arabidopsis. Brassicales; Brassicaceae; Arabidopsis. 1 (sites) AUTHORS Raneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. TILE Squance features of Arabidopsis thaliana chromosome 3. II. Squance features of the 4,251,695 bp regions covered by 90 Pl, TAC and BAC clones JOURNAL DNA Res. 7 (3), 217-221 (2000) MEDLINE 2055099 REFERENCE 2 (bases 1 to 82360) AUTHORS Raneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S. TILE Direct Submission JOURNAL Institute, Department of Plant Gene Research Institute, Department of Plant Gene Research Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamugkazusa.or.ip,	Tel:81-438-52-3935, Fax:81-438-52-3934) COMMENT Address for correspondence kaos@kazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgl.bin/agd_graph.cgl?c=MYO24 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (informatics Group, Oak Ridge National Laboratory, http://compbio.orni.gov/Grail-13/), GENSCAN (Chris Burge, MIT, http://cCR-081.mit.edu/GENSCAN.html), NetCenece (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://grenlini.com/ain.html.com/ain.html).	Can Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5 clone is MWE13 and the 3 clone is T13310. The 5 clone is MWE13 and the 3 clone is T13310. The 5 clone is MWE13 and the 3 clone is T13310. FEATURES 1

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KAILPLSMYFPPSEYVKKIKLSIRCYTHEVLTTFDKLEPEMSKSEREWPONHPSFQHI
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KHQEWVRNVIHHIGSISRLPSCIYLLSHGETDRRSVRPNGDSMDNQRESPRWEPMDKT
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EGFRLMRKVIILDGTHMKTAYGGILIVATTQDPVHSRCASPWECARAYTEAEFLRCYF
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                                                                                                                                         1199 CGGTGAAGCAAGAATACTGTCGATTGATGGAGAAGGTTTACGATGTCGTTGTGAAAC 1258
                                                                                                                                                                                                           1259 CGAGGGATGCTGCCGGAGGATTGGAGTTGTCTTTGCCAAAGGAGGAATTGCAAG 1318
                                                                                                                                                                                                                                                                             1319 CTTTTGATGATTATTTTGCGGAGGGAATAAAGGGTTGATTAATCATTAATCATGTATTA 1378
                                                                                                                                                                                                                                                                                                                                                 1379 TGAAGTTGGATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAATAATTTTTTCCATT 1438
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Length 82360;
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4.6%; Score 69.6; DB 13;
52.0%; Pred. No. 0.00037;
live 0; Mismatches 164;
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                   Similarity
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Perfect score:

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Human osteopontin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product- Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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                                                                                                                                                                                                                                                       AAC51043
AAC42550
AA011712
AAZ20056
AAN90224
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AAQ11712
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AAQ27886
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                                                                                                  AAF58238
AAC64785
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AAZ23902
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17-FEB-1995;
29-JUN-1995;
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                                                                                                                  (without alignments)
2145.203 Million cell updates/sec
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                                                                                                                                                      November 5, 2001, 18:11:58; Search time 445.49 Seconds
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(*SIDSI_/gcgdata/geneseq_/geneseq_NAl980_DAT:*

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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       730101 segs, 313950809 residues
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Maximum Match 100%
Listing first 45 summaries
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AAT37311
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AAF58259
AAF58259

    nucleic search, using sw model

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                                                                                                                      with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313. NOTE: This sequence is supposed to cross reference with the protein described in AAM04727, however there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide given in the specification and described in AAW04727 that the indexer decided
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                            57
                                                  plants
tone,
                                                                                                               containing DNA fragments encoding proteins of plant origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                   CTAGCGACGATTATGAAGATCTCCAGCTGCCGCCGATAGTCGAGGAATCTGATCGGAAAT
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                                                                                                                                                                                                                                                                                                                       2 TGACCACCCTCCTCGAATCCTCCGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAATCCTTATCTCTAACCCTCAAACACTTCTTCCCCCTTTCATGCAATCTAATCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGAA
                                                                                                                                                                                                                                                                                Length 1518;
                                                  transforming
ering colour
                                                                                                                                                                                                                                                                                                    Indels
 Mizutani
                                                                                                                                                                                                                                                  Sequence 1518 BP; 384 A; 340 C; 366 G; 428 T; 0 other;
                                                acyl transferase – for transf
in pigments and thus altering
                                                                                                                                                                                                                                                                               98.9%; Score 1505; DB 17; 99.8%; Pred. No. 1.2e-278;
                                                                                                                                                                                                                                                                                                    ;
0
Kusumi T,
                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                         which produce anthocyanin pigments and e.g. of flowers
                                                                                         Claim 4; Page 73-76; 94pp; Japanese
Ashikari T, Fujiwara H, Fukui Y,
Nakao M, Tanaka Y, Yonekura K;
                                                                                                                                                                                                                               to cross reference the two.
                                                                                                                                                                                                                                                                                          Best Local Similarity 99.8
Matches 1518; Conservative
                                                  for aromatic
                            WPI; 1996-393401/39
                                                  coding
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ACGCGCAGAAACGTCCGTTGGAATCGCAGCATCCATCTTTACCGACGGATCGGATTCGAG
             CTACCTACCTTTTCACCCCAATCTGAAATTAAGAAATTGAAGGGTTTGATTCAGAGAAAG
                                                                              CCCCAAATGTAGTTAATCTCTTCCTTCGTCGCGATCGCAGCTTATATCTGGACCGGCA
                                                                                                                                               TTCCGATCGATTTAAGGCCGCGTTTGGATCCGCCGGCTCCGGGGAACTACTTCGGAAACT
                                                                                                                                                                                                                                                                                                                              GTCTATCGTTTGCGATGCCGAAGATCCTGCGGCGGGATTTGGTCGGAGATGAAGGGGTGT
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CTTCCATCACTAAATTCGGAGGAGATGATGAATTCTTGGACGGAAAAGGTGAATGTTTGC

TAACGACGCACACACCGTTAGCGATGCTCCATCGTTTGTAGGGTTTATGAAGAGTTGGG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                  plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTCTCGGAATCCTCCGGAGTGGCGCCCTCCAGGCACGGTGGCTGAGCAGTCACTCC
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Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentlana triflora; Petunia hybrida; Perilla ocimoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 1479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                              coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour of flowers
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                                                                                                                                                                                                                                                                                                       Mizutani
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                                                                                                                           Aromatic acyl transferase.
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es 417;
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                                      Lavandula angustifolia; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 765.4; D
Pred. No. 1.6e-
1; Mismatches
                                                                                                                                                                                                                                                                                                       Kusumi
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 65-69; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                       χ,
                                                                                     Location/Qualifiers
                                                             Perilla ocimoides (Clone pSAT208)
                                                                                                                                                                                                                                                                                                      ', Fujiwara H, Fukui
Tanaka Y, Yonekura K;
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95JP-0067159.
95JP-0196915.
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Best Local Similarity 71.1%;
Matches 1056; Conservative
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P-PSDB; AAW04725.
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                                      Scenecio cruentus;
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17-FEB-1995;
29-JUN-1995;
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aagatgcagtcccttctcttttacgactttccgtacccaagaacacatttcttggacact 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                     Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentlana triflora; Petunia hybrida; Perilla ocimoides;
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                 Mizutani
       Sequence 1703 BP; 512 A; 353 C; 356 G; 482 T; 0 other;
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/product= Aromatic acyl transferase.
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                                                                                                                                                                                                                                                                                                                                                                                           Kusumi T,
                                                                                                                                                                                  Scenecio cruentus; Lavandula angustifolia; ds
                                                                                                                                                                                                     Gentiana triflora var. japonica (Clone pGAT4)
                                                                                                                                   Aromatic acyl transferase coding sequence.
                                                                            ВP
                                                                         AAT37308 standard; cDNA to mRNA; 1703
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6..1415
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Nakao M, Tanaka Y, Yonekura K;
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DB 17; Length 1703;

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Query Match Best Local Simi Matches 686;

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46 ACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCGACATGACGTGGCTGCATTTCCAC 105

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                                                     Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six appecific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
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                   1207 CAAGAGATACTGTCGATTGATGGAGAGAGTTTACGATGTCGTTGTGTAAACCGAGGGAT
                                           GCTGCCGGAGGATTGGATTGTCTTTGCCAAAGGAGGAATTGCAAGCTTTTGAT
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3..1367
-/*tag = //*tag = //product - Aromatic acyl transferase.
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                                                                                                                                              AAT37312 standard; cDNA to mRNA; 1508
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashikari T, Fujiwara H, Fukui
Nakao M, Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                     Senecio cruentus (Clone pCAT8)
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95JP-0067159.
95JP-0196915.
                                                                              GATTATTTGCGGAGGG 1343
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P-PSDB; AAW04726.
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Score 174.2; DB 17; Length 1508; Pred. No. 1.1e-24;

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Query Match Best Local Similarity

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TACTTCGGAAACTGTCTATCGTTTGCGATGGCGAAGATCCTGCGGCGGGATTTGGTCGGA 1008
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                                              62
ACCCTCCTCGAATCCTCCLGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAGAAAAGCCCCCAAATGTAGTTAATCTCTTCCTTCGTCGCGATCGCAGCTTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         774 ttaacccaagtgccaaacttggagtacatgtcatcttttacggtaacttgtggttatata
                                                                                                                                                                                                                                                                                                                                      TCGCCGG------AGAAAATGCCGGAGTTCCGGTATCAGAACGGTGACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCATCGGAATAACGACGCACCACACCGTTAGCGATGCTCCATCGTTTGTAGGGTTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATGTTTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCTAAATTGGACATAT
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                                                   aacattctcgaacatgccugaatatcggcccctcgggcaccatcggccatcgctcgtta
                                                                                                                                                                                                         TACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gttgtggttacttttgcagaatgttgtcttgactttaataatttgacaggaaatcatcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCGATAGTCGAGGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAGTTGGGCTTCCATCACTAAATTCGGAGGAGATGATGAATTCTTGGACGGAAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 834 tggagttgcatagcgaaatcictcgtaaaaataggagaaagaaagggcgaagacgagtta
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GACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGAGATTCGCGAAGCCTTGCAA 1128
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                                                                                                                                                                                                                      caaatggaggcgttttctagcatctttgatgaaggattagagagtcaagtttcattgtag 1367
                                                                                                                                                                                                                                               -----ATCATGTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTGTTTA 1418
                                                                                                                                                                                                                                                                                              TGGGGTAAGGCGGTGAAGCAAGAGATACTGTCGATTGATGGAGAGAGGTTTACGATGTCG
                                                                                                                                                                    1248 ataaatgcaagcaaaacatcagcacaagatcttgaaattggattgagtctaccgagtatg
                                                               tgggggaagccgataaagtatgagactgtttcaatagactataatacgt---cgatttct
                                                                                                                                                TTGTGTAAACCGAGGGATGCTGCCGGAGGATTGGAGGATTGTCTTTGCCAAAGGAG
                         aataaggacggaatcttgaaagatgccgcgagatggcatgaacctttcatgatcccggct
                                                AACTGTTATTTCTCGGGGGGGGATCGAGCAGGCTTGATCTTTACGGCGCGGGATTTTGGA
                                                                                                                                                                                               GAATTGCAAGCTTTTGATGATTATTTTGCGGAGGGAATAAAGGGTTGATTAATCATTTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentlana triflora; Petunia hybrida; Perilla ocimoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag- a
/product- Aromatic acyl transferase.
701..703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAT37309 standard; cDNA to mRNA; 1622
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1322..1324
/*tag= c
/transl_except= AAT e
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95JP-0067159.
95JP-0196915.
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17-FEB-1995;
29-JUN-1995;
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56 atcaaagttcttgagaaatgccgtgttgcgccaccaccggacgccgtcgccgagtttaca 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 CTA---TCGCCGGAGAAAATGCCGGAGTTCCGGTATCAGAACGGTGACTCGGTTTCTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 gtagattcctccgatagaatgccggagttgcgttacaagaaaggggactccgtttcttta 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGATTATGGAGTCTGTCGGAGATCATCCGCATTCCGCTCATAAATACTACTGCTTTGCC 360
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                                                                                                                                                                                                            Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour
                                                                                                               plants
tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ACCACCTCCTCGAATCCTCCCGAGTGGCGCCGCCTCCAGGCACGGTGACTGAGCAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttctacagattccgccatccttgtcccaactcta---aatttatcattcatccattaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 CCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCGATAGTCGAGGAATCTGATCGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 tataaattcaacgatttgattccccagctcccagaacccattgtaacctccggcgacgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 TIGTITCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 ATAACGACGCACCACACGGTTAGCGATGCTCCATCGTTTGTAGGGTTTATGAAGAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gttttggttgacaaatccaatggagattc---attaaagttccttccactttcttctcta
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                                                                                                                                                                                                                                                                                Six
                                                                                                                                                                                                                                                                                                                                                                                              Score 153.8; DB 17; Length 1622; Pred. No. 8.4e-21;
                                                                                                                                                                                                                                                                           tone changes and allowing new colourations to be produced. Sin specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                        which produce anthocyanin pigments and thus altering colour e.g. of flowers
               Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                 Mizutani
                                                                                                                                                                                                                                                                                                                                              Sequence 1622 BP; 478 A; 354 C; 313 G; 477 T; 0 other;
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               Kusumi T,
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               Fukui Y,
             ľ, Fujiwara H, Fukui
Tanaka Y, Yonekura K;
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                                                             WPI; 1996-393401/39
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                              P-PSDB; AAW04723
               Ashikari T,
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                                Nakao M,
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                                                                                                                                                                                                                                                                        ATCCTGCGGCGGGATTTGGTCGGAGATGAAGGGGTGTTTCGGGCAGCTGAGGCGATCGCG 1044
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             710 gaaagaaaactgctcaaatctcagggcacacctactgttctaaatccagcaatttctaaa 769
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                                                           gatgaagttcgagccaccttcatcctacaccctattgatatcatgaagctcaagaaattc
                                                                                                       atttcgtcaaaaaatcgcaacttaaccggtagtagtaattataatctgtcaactttcacg
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                                                                                 ATTCAGAGAAAAGCCCCAAATGTA--------GTTAATCTCTTCCTTCGTC
                                                                                                                              814 GCGATCGCAGCTTATATCTGGACCGGCATCGCCAAAT-----CGGTCGGAGATTAC
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                                   GATCGGATTCGAGCTACCTTTTCACCCAATCTGAAATTAAGAAATTGAAGGGTTTG
                                                                                                                                                                                                                                                                                                                                                                   CCGTCTGAGATTCGCGAAGCCTTGCAAAACT-----GTTATTCTCGGTGGCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1430 tttacgaatttcatcaatagt 1450
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990 GCGGCGGGATTTGGTCGGAGATGAAGGGGTGTTTCGGGCAGCTGAGGCGATCGCGGCGGA 1049
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                                                                                                                                                                          Nucleic acids containiny electron-transfer group, useful as labels i
hybridization assays, e.g. for genotyping, allowing repeat analyses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 87; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.7%; Score 87; DB 22; Best Local Similarity 6.2%; Pred. No. 4.3e-08; Matches 33; Conservative 295; Mismatches 20
                                                                                                                                                                                                                                                                                                   Example 6; Page 127; 159pp; English
(CLIN-) CLINICAL MICRO SENSORS
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                                                                                                               WPI; 2001-159728/16
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                     Query Match 5.7%; Score 87; DB 22; Length 93
Best Local Similarity 6.2%; Pred. No. 4.3e-08;
Matches 33; Conservative 295; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                             ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                             Electron-transfer group;
                                                                                                                                                                      AAF58257 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                               gene expression; ss
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6.2%; Pred. No. 4.3e-08;
Live 295; Mismatches 205; Indels
                                                   Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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17-MAR-2000; 2000US-0190259
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Best Local Similarity 6.2%
Matches 33; Conservative
                 Oligonucleotide D1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single surface
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                                                                                                             Synthetic.
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1050 AATAGAGAAGAGGACGAGGACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGA 1109
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                                                                                                                                                                                                                                                                                                                                           The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having
 1110 GATTCGCGAAGCCTTGCAAAACTGTTATTTCTCGGTGGCGGGATCGAGCAGGCTTGATCT
                                                                                                                                                                                                                 1170 TTACGGCGCGCGGATTTTGGÄTGGGGTAAGGCGGTGAAGCAAGAGATACTGTCGATTGATGG
                                                                                                                                                                                                                                                                                   group; ETM; mismatch; genotyping;
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AAF58262/c
ID AAF58262 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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1230 AGAGAAGTTTACGATGTCGTTGTGTAAACCGAGGGATGCTGCCGGAGGATTGGAGGTTGG 1289
                                                                                                                                       1350 GGGTTGATTAATCATTAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTC 1409
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                                  1290 ATTGTCTTTGCCAAAGGAGGAATTGCAAGCTTTTGATGATTATTTTGCGGAGGGAATAAA
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gene expression; ss.
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17-MAR-2000; 2000US-0190259
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                                                                                                                                           1050 AATAGAGAAGGACGACGACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGA 1109
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                                                                                                                                                                                                                                                                                                                                                               different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nuclectide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                       1110 GATTCGCGAAGCCTTGCAAAACTGTTATTTCTCGGTGGCGGGATCGAGCAGGCTTGATCT
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                                                                     5.7%; Score 87; DB 22; Length 93 larity 6.2%; Pred. No. 4.3e-08; Conservative 295; Mismatches 205; Indels
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                                           Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other
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AAF58255 standard; DNA; 938
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17-MAR-2000; 2000US-0190259.
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                                                                             Local Similarity
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Best Local S
Matches 33
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1050 AATAGAGAAGAGGACGAGGGACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGA 1109
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Conservative 295; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
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4.3e-08;
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                                                                                                                                                                                                                                                                 Example 6; Page 127; 159pp; English
(CLIN-) CLINICAL MICRO SENSORS INC.
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nes 33; Conserv
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
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17-MAR-2000; 2000US-0190259.
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 Oligonucleotide D1875
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Electron-transfer group; ETM; mismatch; genotyping;
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5.3%; Score 80.2; DB 22
Best Local Similarity 1.3%; Pred. No. 8.6e-07;
Matches 4; Conservative 219; Mismatches 95
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                                                                                                                                                                                                                                                                (CLIN-) CLINICAL MICRO SENSORS INC.
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17-MAR-2000; 2000US-0190259
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                 gene expression;
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Length 936; Indels 1387

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                                   ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                      Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                            hybridization assays, e.g. for genotyping,
                                                                                                                                                                                                                     electron-transfer
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                                                                                                                                                               (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                   26-JUL-2000; 2000WO-US20476.
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(first entry)
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                                   Electron-transfer group;
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                 Oligonucleotide D1954
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1268 CTGCCGGAGGATTGGAGGTTGGATTGTCTTTGCCAAAGGAGGAATTGCAAGCTTTTGATG 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTATTTTGCGGAGGGAATAAAGGGTTGATTAATCATTTAATCATGTATTATGAAGTTGG 1387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyphng, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAATAATTTTTTTCCATTGAACTTTTT
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                                                                                                         ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
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1.3%; Pred. No. 8.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 219;
                                                                                                                                                                                                                                                                                                                                                        26-JUL-2000; 2000WO-US20476.
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17-MAR-2000; 2000US-0190259.
  (first entry)
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                                                                                                         Electron-transfer group;
gene expression; ss.
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                                                       Oligonucleotide D2004
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a single surface
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24-APR-2001
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                                                                                                                                                                                            Synthetic.
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5, 2001, 18:12:08

Search completed: November

AAF58259 standard; DNA; 936 BP

Job time: 15463 sec

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Sequence 18, sequence 15, Sequence 15, Sequence 19, Sequence 19, Sequence 19, Sequence 3, A Sequence 2, A Sequence

Appl Appl

Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence

Sequence 1 Sequence 2 Sequence 2

Run on:

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-08-813-150-1
US-07-847-010-18
US-07-847-010-18
US-08-481-190-15
US-08-481-190-15
US-08-48-19-19
US-08-248-35-19
US-08-248-35-19
US-09-248-335-19
US-09-248-335-19
US-09-248-335-19
US-09-248-335-19
US-09-248-335-19
US-09-348-35-19
US-09-348-36-19
US-09-348-36-19
US-09-380-200-1
US-09-181-810-1
US-09-182-816-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)883-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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STRANDEDNESS: single
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ADDRESSEE: Foley & L
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; CLONE: pTZgpt-F1s
US-08-232-463-14
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ZIP: 22313-0299
    FILING DATE:
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Sequence 14, Appl
Sequence 1, Appli
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Sequence 1, Appli
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Sequence 2, Appli
Sequence 1, Appli
Sequence 16, Appli
Sequence 16, Appli
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Patent No. 5231168
Sequence 1, Appli
Sequence 1, Appli
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                                                                                                                                                                                                                                              Sequence 2, Al
Sequence 18,
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Sequence 12,
Sequence 43,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-545-196B-10
US-08-545-196B-12
PCT-US95-07201-43
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US-08-330-108-16
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US-09-664-800-1
US-09-665-309-1
US-09-661-569-1
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Maximum Match 100%
Listing first 45 summaries
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    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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3.7%; Score 57; DB 1; Length 7218;
llarity 4.1%; Pred. No. 0.00037;
Conservative 210; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FALKNER, F. G.
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 91 114 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22313-0239
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DI
SOFTWARE: Patentin Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 899149
INFORMAT#ON FOR SEQ ID NO: 14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA
               Local Similarity
nes 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1459 ACTAC 1463
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US-08-232-463-14/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1087 ACTGTGGAGAACTGGCCGTCTGAGATTCGCGAAGCCTTGCAAAACTGTTATTTCTCGGTG 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGGGATCGAGCCTTGATCTTTACGGCGCGGATTTTGGATGGGGTAAGGCGGTGAAG 1206
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                                                                                                                                                                                                                               Length 7218;
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APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG
ONRBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          Query Match 3.7%; Score 56.8; DB 1; Length 7
Best Local Similarity 4.0%; Pred. No. 0.00041;
Matches 16; Conservative 225; Mismatches 157; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10618
FILLING DATE: 20-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
PCT-US96-10618-1
PCT-US96-10618-1
Squence 1, Application PC/TUS9610618
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/000,352
FILING DATE: 20-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SEQUENCE CHARACTERISTICS:
                                          nucleic acid
EDNESS: single
                                                                                                                                 ; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                         linear
                                                                                         TOPOLOGY: 11ne
IMMEDIATE SOURCE
                                                               STRANDEDNESS:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1379 TGAAGTTGGATGAAATCCTCTGTTTCATCTTATTGTTTAAACAATAATTTTTTCCATT 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52.6; DB 5;
Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.5%; Score 52.6; Di
Best Local Similarity 56.7%; Pred. No. 0.00:
Matches 97; Conservative 0; Mismatches
                                                                                                                       PF-0042 PCT
                 APPLICATION NUMBER: 08/567,817
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                          NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/07867106
Patent No. 5389526
                                                                                                                                                                                                                                                                                                                                                                                        Rheumatoid Synovium
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feeney, Joanne Longo
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
PRIOR APPLICATION DATA:
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MOLECULE TYPE: CDN
IMMEDIATE SOURCE:
LIBRARY: Rheumat
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,677
                                                                                                                                                                                                                                                       3.4%; Score 51.4; DB 1;
ilarity 59.1%; Pred. No. 0.0054;
Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RICE-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-789-1400
TELEFAX: 713-789-2679
             REFERENCE/DOCKET NUMBER: RITELEDOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
35,134
                                                                                                                                                           TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 1:
                                                                                                         LENGTH: 3138 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 5173 base pairs
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STRANDEDNESS: single
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 77210
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houston
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                                                                                                                                                                                            ; ANTI-SENSE:
US-07-867-106-4
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1859 AATGGTTTAAAAAAACTTGGGTTGGTTAATTATTATTTGAAAATTTTAAAAACCCAAATTA 1918
 Gaps
                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GAPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C
APPLICANT: Chang, Andy C
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Inproved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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Pred. No. 0.014;
0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106 FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   ; Sequence 4, Application US/07867106
; Patent No. 5389526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
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Best Local Similarity 65.2%;
Matches 73; Conservative
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MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular
                                      1514 TTTTTTTT 1522
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US-07-867-106-4
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                                                                                                                                                                                                                                                                             1388 ATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAATAATTTTTTTCCATTGAACTTTTT 1447
                                                                                                                                                                                                                             5042 ATAAACACTTTTTGTTAAATTGTATTCTTCCTTTAATAAAATATTTTAAGCAATTGTCCA 5101
                                                                                                                                                                        Gaps
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;Patent No. 5198345
; APPLICANT: GWYNNE, DAVID I.;BUXTON, FRANCIS P.;PICKETT, MARK H.;DAVIES, ROGER W.;SCAZZOCCHIO, CLAUDIO
TITLE OF INVENTION: VECTORS IN USE IN FILAMENTOUS FUNCI
NUMBER OF SEQUENCES: 28
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5198345-15
Patent No. 5198345
APPLICANT: GWYNNE, DAVID I.; BUXTON, FRANCIS P.; PICKETT, MARK
DAVIES, ROGER W.; SCAZZOCCHIO, CLAUDIO
TITLE OF INVENTION: VECTORS IN USE IN FILAMENTOUS FUNGI
NUMBER OF SEQUENCES: 28
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.3%; Score 49.8; DB 6; Length 130; 82.6%; Pred. No. 0.0044; tive 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 130;
                                                                                                                              3.3%; Score 50; DB 1; Length 5173; 56.8%; Pred. No. 0.013; tive 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                 3.3%; Score 49.8; DB 6;
82.6%; Pred. No. 0.0044;
tive 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/811,404
FILING DATE: 20-DEC-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/811,404
FILING DATE: 20-DEC-1985
                                                                                                                                                 Best Local Similarity 56.8
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 82.6
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.3
Best Local Similarity 82.6
Matches 57; Conservative
MOLECULE TYPE: CDNA
                                                      1..4863
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                                 ; NAME/KEY;
; LOCATION:
US-08-242-677-1
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                                                                                                                                Query Match
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Sequence 1, Application US/09664800
Patent No. 6218527
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Abscistc Acid Responsive Element -Binding Transcription Fac
FILE REFERENCE: 1942/42
CURRENT APPLICATION NUMBER: US/09/664,800
CURRENT FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/416,050
PRIOR APPLICATION NUMBER: 09/416,050
PRIOR FILING DATE: 1999-110-12
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09665309
Sequence 1, Application US/09665309
Sequence 1, Application US/09665309
Sequence 1, Application US/09665309
GENERAL INFORMATION:
APPLICANT: KIM. Soo Young
TITLE OF INVENTION:
APPLICANT: APPLICATION NUMBER: US/09/665,309
CURRENT APPLICATION NUMBER: 09/416,050
PRIOR PILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
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Pred. No. 0.014;
0; Mismatches 33; Indels
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                                                                                     FastSEQ for Windows Version 4.0
                                                                                                                                               ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-416-050A-1
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US-09-664-800-1
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 67.6%;
Matches 69; Conservative
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Best Local Similarity
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SEQ ID NO 1
LENGTH: 1578
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LENGTH: 1578
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US-09-416-050A-1
; Sequence 1, Application US/09416050A
; Sequence 1, Application US/09416050A
; GENERAL INFORMATION:
; APPLICANT: KIM. Soo Young
; TITLE OF INVENTION: Absclist Acid Responsive Element -Binding Transcription Factors
; FILE REFRENCE: 1942/42
; CURRENT APPLICATION NUMBER: US/09/416,050A
; CURRENT FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 83
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APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPENDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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Pred. No. 0.017;
0; Mismatches 29; Indels 0
                                                                                                                                                                                                                                                                                                                                  CUP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: 35,134
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
FILING DATE: 215-568-3100
TELEPHONE: 215-568-3139
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEDPHONE: 215-568-3439
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEDPHONE: ALIBER ACTION STRANDEDNESS: SINGle
TYPE: NUCLEC ACID
STRANDEDNESS: SINGle
TYPE: Linear
TOPOLOGY: DAM (Genomic)
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Best Local Similarity 69.89
Matches 67; Conservative
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2378..5038
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; LOCATION:
US-07-867-106-2
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LOCATION:
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1364 TTTAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAA 1423
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61.1%; Pred. No. 0.016;
tive 0; Mismatches 49;
                                                                                                                         Sequence 16, Application US/08330108
| Patent No. 5795752
| GENERAL INFORMATION:
| APPLICANT: Smith, Kendall A. TITLE OF INVENTION: IL-2-Stimulated General Fire OF INVENTION: Expression NUMBER OF SEQUENCES: 20
| CORRESPONDENCE ADDRESS: ADDRESSEE: Lahive & Cockfield |
| STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: November 5, 2001, 18:05:10 Job time: 15110 sec
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APPLICATION NUMBER: US/08/104,736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: US/07/796,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,108
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 base pairs
TYPE: nucleic acid
STRANDEDNESS: single stranded
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE: T-cell blast
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Best Local Similarity 61.19
Warches 77; Conservative
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COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
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CITY: Boston
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                                                                                            RESULT 15
US-08-330-108-16
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ROBEY, PAMELA G
TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FILING DATE: 03-NOV-1989
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                                                      DB 4; Length 1578;
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                                                    3.2%; Score 49.2; DB 4; Length 167.6%; Pred. No. 0.014;
tive 0; Mismatches 33; Indels
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Pred. No. 0.014;
0; Mismatches 33; Indels
                                                                                                                                                                                                   FILE REFERENCE: 1942/42

FILE REFERENCE: 1942/42

CURRENT APPLICATION NUMBER: US/09/661,569

CURRENT FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 09/416,050

PRIOR FILING DATE: 1999-10-12

NUMBER OF SEQ ID NOS: 83

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1578
                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09661569
Patent No. 6245905
GENERAL INFORMATION:
APPLICANT: KIM. Soo Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana US-09-661-569-1
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Best Local Similarity 67.6%;
Matches 69; Conservative
                                                  Query Match 3.2%
Best Local Similarity 67.6°
Matches 69; Conservative
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5340934-5
;Patent No. 5340934
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US-09-665-309-1
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(without alignments)
2473.399 Million cell updates/sec
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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9b_est2:**

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9b_est13:**

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Perfect score:
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	200: em_gss_humf:: 201: em_gss_humf:: 202: em_gss_humf:: 203: em_gss_humf:: 204: em_gss_lnv1:: 205: em_gss_lnv2:: 206: em_gss_lnv3:: 206: em_gss_lnv3:: 207: em_gss_lnv1:: 208: em_gss_pln1:: 209: em_gss_pln1:: 209: em_gss_pln2:: 210: em_gss_pln2:: 211: em_gss_prod:: 212: em_gss_rod2:: 213: em_gss_rod3:: 214: em_gss_rod3:: 215: em_gss_rod3:: 216: em_gss_rod3:: 217: em_gss_rod3:: 218: gb_gss3:: 218: gb_gss3:: 220: gb_gss3:: 221: gb_gss3:: 222: gb_gss6:: 222: gb_gss6:: 223: gb_gss6:: 224: gb_gss6:: 225: gb_gss8:: 226: gb_gss8:: 227: gb_gss8:: 227: gb_gss8:: 228: gb_gss8:: 229: gb_gss8:: 220: gb_gss8:: 2	
9b_est48:* 9b_est48:* 9b_est50:* 9b_est51:* 9b_est53:* 9b_est53:* 9b_est55:* 9b_est56:*	99-est59:* 99-est50:* 99-est50:* 99-est60:* 99-est60:* 99-est60:* 99-est65:* 99-est65:* 99-est76:* 99-est76:* 99-est89:*	gb_est66:* gb_est70:* gb_est71:* gb_est71:* gb_est71:* gb_est73:* gb_est91:* gb_est91:* gb_est93:* gb_est193:* gb_est103:* gb_est103:* gb_est103:* gb_est109:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

allenged w	For clone info: picase contact Research Genetics, Libraries Division tel 1-800.711-6195, email cdna@resgen.com Seq primer: M13P-R. Location/Qualiflers 1. 763 /organism="Solanum tuberosum" /cultivar="Kennebec" /db_xrefe="texton:4113" /clone="HPLIDAA4" /clone="HPLIDAA4" /clone="HPLIDAA4" /fissue_type="leaf" /dev_stage="6 week old" /lab_host="SolR" /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Whole plants were challenged with 450,000 sporangia/ml P. infestens US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestens US-1) were used as controls and showed infeature US-1; were used as controls and showed	act act 3		264 GGAGTTCCGGTATCAGAACGGTGACTCGGTTTTTCACGATTATGGACTCTGTCGGAGA	OY 444 AGRACTOSTITCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	1 159 10.4 763 155 BG59947 BG59947 EST499600 157.2 10.3 690 155 BG59947 BG59947 EST504342 146.6 9.6 606 113 AW221049 BG59947 EST504342 146.6 9.6 606 113 AW221049 BG59947 EST207518 EST207518 138.8 9.1 583 113 AW221050 BE922784 EST425553 138.8 9.1 584 142 BE922746 BE922746 BE922746 EST425179 123 8.1 574 142 BE922746 BE922746 BG992765 EST425179 119.4 7.8 508 173 BG097054 EST4061573 110.4 7.8 508 173 BG097054 BG997054 EST4061573 110.4 7.8 508 173 BG097054 EST4061573 110.4 7.8 591 155 BG598154 AW650280 EST307054 EST4061573 110.4 518 119 AW650280 EST307054 EST406157 110.4 518 119 AW650280 EST307054 EST406157 110.6 591 155 BG598154 AW650280 EST307054 EST406157 110.6 591 155 BG598154 BG9999 BG99959 EST400516 BG99237 EST4061734 110.6 591 154 AF6 142 BE922378 BG99237 EST40519 110.6 591 154 AF6 142 BE922378 BE922379 BC9709	86 5.7 4.08 14.2 BE920022 BE920022 85.8 5.6 354 14.2 BE922950 BE922950 85.4 5.6 703 14.3 BF0522950 BE922950 85.2 5.6 703 14.3 BF0522950 BF0522950 84.8 5.6 490 110 AW038715 AW038708 81.8 5.4 409 111 AW033479 AW038479 81.8 5.4 788 164 BE187619 BE187619 79.2 5.2 597 120 AW74948 BF642724 79 5.2 656 119 AW692527 AW642527	79 5.2 677 118 AW586972 AW586972 77.2 5.1 318 BE660849 BE660849 77.2 5.1 311 166 BE53747 BG562734 77.2 5.1 311 166 BE53747 BG532201 75.6 5.0 334 AV440958 AV440958 71.6 4.7 1101 219 CNS00293 AL097377 71.2 4.7 676 153 BG455847 BG455847 70.2 4.6 526 166 BE323055 BG55867 70 4.6 422 155 BG589694 BG586969 69.8 4.6 694 117 AW500686 AW500686		CREATION TOTALISM LUBERSONING TOTAL STREET S

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Alcala,J. Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Upublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLEF - Fruit were tagged at the lon stage and harvested 5-6 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST297518 tomato fruit mature green, TAMU Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seeds and locules were discarded prior to freezing the
  TTCAATTATCTCATTGGTGACCATCGGCGTAATGCTAAGGATTTTTATCACTTTGTTCT 368
                                                                                                             369 ACGTTAGGGGAACCTAAGGATGCACCCGGGGTCCAATTAGCTCCGGTCTTAGCCATTCAA 428
                                                                                                                                                        GTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGAATAACGACGCACCACACGGTTAGC 504
                                                                                                                                                                               505 GATGCTCCATCGTTGTAGGGTTTATGAAGAGTTGGGCTTCCATCACTAAATTCGGAGGA 564
                                                                                                                                                                                                                                                                      07-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. :606
/organism="Lycopersicon esculentum"
/oultivar="TA496"
/db xref="taxon:4081"
/clone="CLEF3F1"
/clone=lb="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                  385 CAGCTGCCGCCGATAGTCGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 113; Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.6%; Score 146.6; DB 113; Lengt
Best Local Similarity 53.4%; Pred. No. 2.6e-20;
Matches 308; Conservative 0; Mismatches 269; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
TRI: 864 656 436
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA clone cLEF3F1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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143 c
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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                      309
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JOURNAL
COMMENT
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1 (bases 1 to 690)

2 van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes

Unpublished (2000)

Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries Division tel 1-800-111-6195, email cdna@fesgen.com
Seq primer: MIBF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhOI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                          EST504342 cSTS Solanum tuberosum cDNA clone cSTS25122 5' sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCCGCATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 AAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 ATGACGTGGCTTTTCCACCCCATGCTTCAGCTTCTCTTCTACGAACTCCCCTGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 155; Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 157.2; DB 155; Lengtl
Pred. No. 1.7e-22;
0; Mismatches 248; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="texon:4113"
/clone="cSTS5122"
/clone="cSTS7"
                                                                                                                                                        mRNA
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55.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tubers.
                                                                                                                                                                                                    mRNA sequence.
BG599447
564 AGATGATGAATTCTT
                         544 AGATGAACAATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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KEYWORDS SOURCE ORGANISM

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FEATURES

REFERENCE AUTHORS

LOCUS DEFINITION

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Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Llang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in light attraces.
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae: euasterids I; Solanales; Solanaceae; Solanum;
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AW221050
AW221050.1 GI:653:734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CACTCCCGCTCACCTTCTTCGACATGACGTGCTTGCATTTCCACCCCATGCTTCAGCTTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AACAATCCTTAFCTCTAACCCTCAAACACTTCTTCCCCCTTTCATGCAATCTAATCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 AGGATTTTTATCACTTTGTTCCTACGTTAGGGGAACCTAAGGATGCACCGGGGTCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 TGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                             2 TGACCACCCTCCTCGAATCCTCCCGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGT
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                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                   252; Indels
                                                                                                                                                                                                                                                                                             DB 142;
                                                                                                                                                                                                                                                                                                                        le-18;
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                          Score 138.8;
Pred. No. 1e-
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                                                                                                                                    liquid nitrogen."
                                                                                                                                                                                                                                                                                          9.1%;
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                                                                                                                                                                                                                                                                                                                                                   290; Conservative
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| Spermatophyta: Magnollophyta; eudicotyledons; core eudicots:
| Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
| Ichaesa 1 to 570)
| SS van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
| Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning
| C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
| Experimentation of Estra from potato leaves and petioles
| C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
| Contact: Cathy Ronning
| The Institute for Genomic Research
| For clone request: please contact Research Genetics, Libraries
| Division tel 1.800-11-6195, email cdna@resgen.com.
| Location/Qualifiers
| Location/Qualifiers
| Location/Qualifiers
| Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Quali
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                                                                                          CACTCCCGCTCACCTTCTTCGACATGACGTGGCTGCATTTCCACCCCATGCTTCAGCTTC 121
                                                                                                                                             65 TACTCCCTCTTACTTTTGACCATGTTTGGTTAGGGTTTCGCCGTATGAGGCGGATAT 124
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      122 TCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCA
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/db_xref="taxon:4113"
/clone="csTB22E2"
/clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                        /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Shol; cEEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the
                                                                                                                                                                                                                                                                                                                                                                    seeds and locules were discarded prior to freezing the
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                                                                                                                                                                                                            /db_xref="taxon:4081"
/clone="cLEF3F3"
/clone="Lb="town fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev.stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 AACAATCCTTATCTCTAACCCTCAAACACTTCTTCCCCCTTTCATGCAATCTAACTACC
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                                                                                                                                                                                 /organism="Lycopersicon esculentum"/cultivar="TA496"
 tomato fruit tissue
            Unpublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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1 (bases 1 to 56,1)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of ESTs from potato leaves and petioles
Uppublished (2000)
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                             \rm EST425179 potato leaves and petioles Solanum tuberosum cDNA clone cSTB13B18 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cathy Rouning
Contact: Cathy Rouning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdnafresgen.com.
Location/Qualifiers
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02-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 124.8; DB 142; Lengt
Pred. No. 7.9e-16;
0; Mismatches 242; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib-"potato leaves and petioles"
/tissue_type-"leaflets and petioles"
/do_stage="8 weeks old plants"
/lab_host="SolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB13B18"
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Notice: Shoemaker, R. Kedin, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, Shoemaker, R., Kedin, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Svaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Kitter, E., Kohin, S., Shin, T., Jackson, Y., Cardenas, M., McCann, Public Soybean EST Project
Unpublished (1999)

Public Soybean EST Project

Contact: Shoemaker R/Public Soybean EST Project
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This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
Asxway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Maynoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhOI; The mRNA was isolated from entire roots of 2-month-old 'Williams' plants that were greenhouse grown in 5-gallon potes. To suppress nodulation, Black Gold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW102336 687 bp mRNA EST 21-NOV-2000 sd86d06.yl Gm-c1009 Glycine max cDNA clone GENOME SYSTEMS CLONE Gm-c1009-1284 5' similar to TR:Q92WB4 Q92WB4 F21M11.13 PROTEIN.
                                                                                                                                                                                                                                                                                         300 TAAGGATGCACCGGGGGTCAAACTAGTCCCGGTCTTAGCCATTCAAGTGACACTTTTTCC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                    360 GAATCTTGGCATATCCGTTGGTTTTAGTAACCATCATGTCGCTTGTGAAGGAAATACCAT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Farkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                             339 TCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCGAT
                                                                                                                                                                               243 TGGTAACCATCCTCGAAATG --- CTAAGGATTTTTATCCCATTCCTCAATTGGCACAACC
                                                                                                                                                                                                                                                                                                                                                                                                459 CGGTCGCGGGGTGTGCATCGGAATAACGACGCACCACCACCGTTAGCGATGCTCCATCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       519 TGTAGGGTTTATGAAGAGPTGGGCTTCCATCACTAAATTCGGAGGAGATGATGTTTTT
                                                                                                                                                                                                                                                     399 AGTCGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCC
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/db_xref="taxon:3847"
/clone="GBNOME SYSTEMS CLONE ID: Gm-c1009-1284"
/clone=_ilb="Gm-c1009"
/lab_host."XL10-Gold"
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Insert Length: 2097 Std Error: 0.00
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High quality sequence stop: 431.
Location/Qualifiers
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For act of Contact: Cathy Rouning

The Institute for Genomic Research Genetics, Libraries

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE922746 574 bp mRNA EST 02-OCT-2000 EST426515 potato leaves and petioles Solanum tuberosum cDNA clone cSTB21L12 5' sequence, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 CTTAGCTGGCAACATTGCTTGTCCACTAAATTCGAGTGGTTATCCTGAGTTGCGTTATGT 182
                                        457 ACACTTTTCCGAATCTTGCCATATCCGTTGGTTTTAGTAACCATCATGTCGCTTGTGAT 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 TITCCACCCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCT 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
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388 CTGCCGCCGATAGTCGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 574;
                                                                                                                                                                                                                                                                                  508 GCTCCATCGTTTGTAGGGTTTATGAAGAGTTGGGCTTCCATCACTAAA 555
                                                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 1.9e-15;
0; Mismatches 215;
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Best Local Similarity 54.9
Matches 265; Conservative
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ID:

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        ALI-Purpose potting soil was supplemented with: 0.38g/L available phosphoric acid (P205), 20mg/L urea N. 0.16g/L S. 0.49mg/L Br. 2.5mg/L Cu. 0.15g/L Fe, 13.53mg/L Mn. 0.20mg/L Mn. 0.20mg/L Mn. 0.20mg/L Ca, and the following nutrients in a slow-release form (Osmocote): 0.165g/L ammonia N. 0.185g/L nitrate N. 0.35g/L available phosphoric acid, and 0.35g/L soluble potash. No nodules were visible on the roots at harvest. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the CDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated CDNA is hemimethylated. Stratagene's first-strand synthesis primer was used (GACAGAGAGACACACACACTCCGAG(T)-18]. After second strand synthesis primer was used (GACAGAGAGACACACACACTCCGAG(T)-18]. After second strand synthesis primer was used with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by disestion with XhoI; all XhoI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 400bp cutoff, using a SizeSep 400 Spun column from Pharmacia. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vith ECORI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with CDNA and mostrs. This library was constructed by Dr. Paul Roll and No. Virgin Column release appear to contain recombinant plasmids with CDNA and phosphorylated Superconted by Dr. Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
All-Purpose potting soil was supplemented with: 0.36g/L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTCAA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACACTTCTTCCCCCTTTCATGCAATCTAATCTACCCTCTATCGCCGGAGAAATGCCGGA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 AGTGGCGCCCCCCCAGGCACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCTTCGACAT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 111; Length 687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 121.8; DB 111; Lengt
Pred. No. 3.3e-15;
0; Mismatches 254; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keim and Dr. Virginia Coryell." 247 \text{ c} 91 q 187 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 52.7
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147
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AGA 566

564

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/note-"vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                potato.
Solanum tuberosum
Eudaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases I to 508)
van der Hoeven, R. S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
                                                           EST461573 potato leaves and petioles Solanum tuberosum cDNA clone cSTB45P9 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCGATTTCGTTCAAACCATTATTCCTACTCTTAAACATTCACTCTCCCTCACTCTCAAA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCGTTATGTGACTGGAGATTCTATATCTGTTACTTTTATTGAGACTGATATGAATTTC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 AATCATCTCATTGGTAACCATCCTCGAAATGCTAAGGATTTTTATCCCTTCATTCCTCAA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTGGCTGCATTTCCACCCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTCCAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTCAAA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCCGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGATCAT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGCATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 GCGCCACCTCCCCACGCGCGCGCACAGAGCTAACGCTCCTCTAACTTATTTTGATCAT 76
                                         29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTTCTTCCCCCTTTCATGCAATCTAATCTACCCTCTATCGCCGGAGAAAATGCCGGAG
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0; Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 119.4; DB 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 508
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB45F9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164
                                            mRNA
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Matches 255; Conservative
                                                                                                                           BG097054.1
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DEFINITION
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                          REFERENCE
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                                                                                                       ACCESSION
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KEYWORDS
SOURCE
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                      BG097054
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TCATGCAATCTAATCTACCCTCTATCGCCGGAGAAATGCCGGAGTTCCGGTATCAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    potato.
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BG598154
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ORIGIN
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 591)
Alcala,J., Vrebblov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum
Starayota, Vitidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                507
                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGCCGTATGAGGCGGATATTTTACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation of ESTs from tomato fruit tissue, breaker stage Unpublished (2000)
Contact: David Frisch
Clemson University
Clemson University
Tion Oordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Email: dfisch@CLEMSON.EDU
                             377 TTGGCACAACCTAAGGATGCACCGGGGGTCAAACTAGTCCCGGTCTTAGCCATTCAAGTG
                                                           ACTCTGTTTCCCGGGTCGGGGTGTGCATCGGAATAACGACGCACCACCGGTTAGCGAT
 CTGCCGCCGATAGTCGAAATCTGAATCTGAAATTGTTTCAAGTTTTAGCCGTGCAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xxef-"taxon.4081"
/clone="cLEG15H6"
/clone_lib="tomato breaker fruit, TIGR"
/tissuc_type="pericarp"
/dev_stage="breaker"
/lab_host="SOLR"

    591
    /organism="Lycopersicon esculentum"
/cultivar="TA496"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 116; DB 167;
52.7%; Pred. No. 5.1e-14;
Live 0; Mismatches 225;
                                                                                                                                                                                                                                                                clone cLEG15H6, mRNA sequence.
BE434257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prime sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                             BE434257.1 GI:9432100
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                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon.
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                                                                                                                                                                                                                                                                                                                               tomato.
                                                                                                                                                      497
                                                                                                                       G 508
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ORIGIN
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                                                                                                                                                                                                                                                DEFINITION
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JOURNAL
COMMENT
 388
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                                                                                                                       508
                                                                                                                                                    497
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BE434257
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Asteridae: euasterids I; Solanales: Solanaceae: Solanum.

E. I (bases 1 to 659)

E. Van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes

I. Unpublished (2000)

Contact: Cathy Ronning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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EST496632 CSTS SOlanum tuberosum CDNA clone CSTS20M23 5' sequence,
mRNA sequence.
BG598154
GGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGATCATCCGCATTCCGCTCAT 342
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/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
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/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="c;rs20M23"
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Best Local Similarity 52.9
Matches 293; Conservative
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum;
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Jaclata, Verbalov, J., White, R., van der Hoeven, R.S, Holt, I.E.,
Liang, F., Hansen, T. S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Glovannoni, J.J., Martin, G.B. and Tanksley
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                          GCGCCACCTCCCCACGCGCGCGCAACAGAGCTAACGCTCCCTCTAACTTTTTGATCT-
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EST328734 tomato germinating seedlings, TAMU Lycopersicon
esculentum cDNA clone cLEI12F13 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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Clemson University
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Contact: David Frisch
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van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E., Liang
,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W.,
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
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51.8%; Pred. No. 3.4e-13;
tive 0; Mismatches 235;
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nes 253; Conservative
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1 (bases 1 to
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Tracheophyta;

endicots

JOURNAL

COMMENT

TITLE

FEATURES

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/note="Vector: pBluescriptSkmcUadapt; Site_1: 5' EcoRI; Site_2: XhoI; Roots were harvested from plants grown under the following deficiencies/stresses: 10 mM Al, Zn, P, K, Fe,N. mRNA was isolated from indivdual treatments. Proportional aliquots of mRNA of each treatment were mixed and used for library construction."
                                                                                                                                                                                1 (bases 1 to 482)
van der Hoeven, R.S., Garvin, D.F., Matern, A.L., Holt, I.E., Liang, F., van der Hoeven, R.S., Garvin, D.F., Matern, M.E., Bowman, C.L., Upton, J., Hansen, T.S., Ronning, C.M., Craven, M.B., Bowman, C.L., and Tanksley, S.D. and Tanksley, S.D. Generation of ESTs from tomato nutrient-deficient roots Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ATGACGTGGCTGCATTTCCACCCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTCC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 AAACCCGATTTCGTTCAAAAJATTATTCCTCTCTTAAAAATTCACTCTCCCTCACTCTC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AAACACTICTICCCCCTITCAIGCAAICTAAICTACCCTCIAICGCGGAGAAAAIGCCG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 CATCCGCATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 AAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTTCCGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 AAACACTATACGCCCTTAGCCGGAAACGTTGCCTTGTCCACTAGATACAAACGGATATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 GAGTTACGTTATGTGACAGGNGATTCTGTGTCTGTTACTTTTTCGAGACTGATATGAAT
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                                                                                     Eŭkaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_11.b="tomato nutrient deficient roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 106.8; DB 144; Lengt
Pred. No. 4e-12;
0; Mismatches 227; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organish="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="roots"
/dev_stage="5-6 weeks old"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="TA492"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: dfrisch@CLEMSON.EDU.
Location,Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="cLEW18020"
                                                                    Lycopersicon esculentum
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Best Local Similarity 51.7%
Matches 243; Conservative
                                                                                                                                                                    ycopersicon.
                                          tomato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded mixture of cells which is highly enriched for trichome likely with minor contaminations of other types of leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST400516 tomato nutrient deficient roots Lycopersicon esculentum CDNA clone cLEW18020 5' sequence, mRNA sequence.
BF096979 GI:10902689
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                                                                                                                                                                                                                                                                                                                                                  /organism="Lycopersicon hirsutum"
/db_xref="taxon:62890"
/clone="cLHTD15"
/tlone_lib="L. hirsutum trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 GCTGCATTTCCACCCCATGCTTCAGCTTCTTTTTACGAACTCCCCTGTTCCAAACCCGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332
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Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from wild tomato (Lycopersicon hirsutum)
tritchomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 GCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCTTCGACATGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TATGCCCTTAGCCGGAAACGTTGCTTGTCCACTAGATACAAACGGATATCCTGAGTTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGATCATCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 TICCGCTCATAAAIACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCGATAGTCGAGGAATCTGATCGCAAATTGTTTCAAGTTTTAGCCGTGCAAGTGACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 TTTTCCGAATCTTGGTGTATCCATTGGTTTCACTAACCATCATGTTGTTGTTGTTGTTGT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCCCCCTTTCATGCAATCTAACCTCTATCCCCGGAGAAAATGCCGGAGTTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.1%; Score 10%; DB 118; Best Local Similarity 51.7%; Pred. No. 2.3e-12; Matches 246; Conservative 0; Mismatches 230;
                                                                           Unpublished (2000)
Contact: David Frisch
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tal: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                   SC 29634, USA
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                                                                                                                                                                                                                                                                                     prime sequence.
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RESULT 1 BF096979

ACCESSION VERSION

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                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Permatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 456)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hanssen, C.L., Doan, B., Bougti, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
                                                                                                                       BEST 72 456 bp mRNA EST 02-OCT-2000 CSTR27341 potato leaves and petioles Solanum tuberosum.cDNA clone CSTB2669 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone request: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 TGCCGTCCTTGATAGAGCAATGTCAAGTTGCGCCACCTCCGGGCGGCGCGCAGCGGAGGTGA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 CACTCCCGCTCACCTTCTTCGACATGACGTGGCTGCATTTCCACCCCATGCTTCAGCTTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 TCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 AACAATCCTTATCTCTAACCCTCAAACACTTCTTCCCCCTTTCATGCAATCTAATCTACC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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1. .456
/organism="Solanum tuberosum"
/organism="Solanum tuberosum"
/cultivar="kennebec"
/db.xref="taxon:4113"
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/clone_lib="potato leaves and petioles"
/tisue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SoLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.4%; Score 97.8; DB 142; Length Best Local Similarity 57.8%; Pred. No. 2.9e-10; Matches 174; Conservative 0; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
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                                                                                                                                                                                                                                               BE923572.1 GI:10449648
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Search completed: November 5, 2001, 18:01:04 Job time: 14904 sec

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Thu Dec

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AF227981 Euphorbia
AL418128 T3 end of
A16155 pTOM36. 10/
A20628 PTOM36 frag
AR003699 Sequence
IZ8271 Sequence
AR110778 Sequence
AR110778 Sequence
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CNSO6W8Q
A16155
A20628
AR003699
IZ8271
AR110778
AF053307
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                                                                November 5, 2001, 16:58:18; Search time 8904.87 Seconds (without alignments) 29:529 Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Submitted (NB-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces extaguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See the other extremity of this insert.
                                  /evidence=not_experimental
/product="F21J9.20-like protein"
/protein_id="AAF34801.1"
/db_xref="G1:684226"
/translation="KRFVFDGSKIGALKEIAASAIAPKPTRVEAVSGLIWKGIITAFK
                                                                                                                         KSNPNLIRPSVWSVSVNLRPRFTPPVPENHACNLVVIVTPKVDEAMELKGLVGVIKOG
MODEVENYVKKVQGEDGVGAICEFGKDFAEKALSDKIDFFMCSGWCRFGLYDADFGWG
KPTWLSIVSTNIRNVCILLDTKDGEGFEAWITLSEEDMSWFESDERVLEFAQVNPGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T3 end of clone AX0AA029C10 of library AX0AA from strain CBS 7064 of ptohla farinosa, sequence tagged site.
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Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Souciet,J.L., Aigle,M., Artiguenave,F., Casaregola,S.,
Belothin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
Benontigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozler-Kalogeropoulos,O., Potler,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of
yeast species for molecular evolution studies(1)
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de Montigny, J., Spéhner, C., Souciet, J., Tekaia, F., Dujon, B., Wincker, P., Artiguenave, F. and Potier, S. Genomic Exploration of the Hemiascomycetous Yeasts: 15. Pichia sorbitophila
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                                                                                                                                                                                                                                                                                                             Length 850;
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1 (bases 1 to 915)
de Montigny,J., Spehner,C., Souciet,J., Tekaia
 GenBank Accession Number AC000103"
                                                                                                                                                                                                                                                                                                         Score 14.2; DB 13;
Pred. No. 9.2e+02;
2; Mismatches 2;
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E12754 Gentianatri
AB026494 Gentiana
AB010708 Gentiana
E12753 Gentianatri
284571 D.caryophyl
116766 Sequence 16
AF228714 Ictalurus
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ABO16892 Arabidops
ACO20525 Drosophil
ACO2014 Homo sapi
ABO20742 Arabidops
ABO13396 Arabidops
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1 (bases 1 to 850)
Anderson,J.V. and Horvath,D.P. Identification of mRNAs expressed in underground adventitious buds of Euphorbia esula (leafy spurge)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP000606 Arabidops
AB023041 Arabidops
AL162508 Arabidops
AB005247 Arabidops
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                                  AX025512 Sequence
AX025518 Sequence
AB029340 Perilla f
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E12757 Senecio cru
Z70521 C.melo mRNA
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E12755 Petunia hyb
 AF190130 Taxus cus
AF190130 Taxus cus
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AC017179 Drosophil
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U32728 Haemophilus
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AF282249 Lactococc
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Direct Submission
Submitted (26-ZAN-2000) Plant Science, USDA/ARS, 1605 Albrecht
Blvd., Fargo, ND 58105, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF227981 850 bp mRNA PLN 17-FEB-2000
Euphorbia esula F21J9.20-like protein mRNA, partial cds.
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/dev_stage="3-day induced (defoliated)"
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/db_xref="taxon:3993"
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AB010708
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I16766
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LLA250129
                 AX025512
AX025512
AX025518
AB029340
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DEFINITION

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RESULT AF227981

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

source

FEATURES

CDS

TITLE JOURNAL

AUTHORS

JOURNAL REFERENCE ö

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Unknown.
Unclassified.
1 (bases 1 to 1080)
Bid,C.R., Boniwell,J.M., Grierson,D., Ray,J.A. and Schuch,W.W.
Transformed tomato plants
Patent: US 5569829•A 1 29-OCT-1996;
                                    Gaps
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Unclassified.
Unclassified.
1 (bases 1 to 1080)
Bird,C.Roger, Grierson,D., Ray,J.Anthony and Schuch,W.Walter.
PTOM36 constructs and tomato cells transformed therewith
Patent: US 5744364-A 1 28-APR-1998;
Location/Qualifiers
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Pred. No. 9e+02;
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Sequence 1 from patent US 5744364.
AR003699
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Sequence 1 from patent US 5569829.
128271.1 GI:1819047
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                                                                                            2 others
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tive 2; Mismatches 2; Indels
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Pred. No. 9.1e+02;
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/db_xref="taxon:32630"
141 c 208 g 375 t
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/db_xref="taxon:32630"
141 c 208 g 375 t
       /organism="Plothia farinosa"
/strain="CBS 7064"
/db_xref="taxon:4920"
/clone="AxOAAO29C10"
/clone_lib="AXOAA"
/note="end : T3"
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1 (bases 1 to 1320)

St-Pierre, B., Laflamme, P., Alarco, A.M. and De Luca, V.

The terminal O-acetyltransferase involved in vindoline biosynthesis defines a new class of proteins responsible for coenzyme A-dependent acyl transfer.

Plant J. 14 (6), 703-713 (1998)
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4101 Sherbrooke East, Montreal, QC H1X 2B2, Canada
Location/Qualifiers
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/product="deacetylvindoline 4-0-acetyltransferase"
/protech_id="AAC99311.1"
/db_xref="GI:4091808"
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17-0-acetyltransferase"
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Pred. No. 9e+02;
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/cultivar="Little Delicata"
/db_xref="taxon:4058"
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St-Pierre, B., Laflamme, P. and De Luca, V.
Direct Submission
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Atkinson, R.L. and Dhurandhar, N.V.
Viral obesity methods and compositions
Patent: US 6127113-A 1 03-0CT-2000;
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Sequence 1 from patent US 6127113. AR110778
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                                                                                                                                                                                                           /organism="unknown"
215 c 227 q
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/translation="MESCKISVETETLSKTLIKPSSPTPQSLSRYNLSYNDQNIYQTC VSVGFFYENPOGIEISTIREQLQNSLSKTLVSSYPPRGKVVKNDYIHCNDDGIEFVEV ALRCRMNDILKVELRSYRADLVLLKRYVGSEDFTAIVQLSHPDGGGAARFGISFHKV ALGCGTTASFMKDWASACYLSSSHHVPTPLLVSDSIFPRODNIICEDFTSRNOVEKT FIFPPEAIEKLKSKAVEFGIEKPTRVEVLTAFLSSCATVAGKSAAKNNNCGQSLPFPV LQAINLRPILELPQNSVGNLVSIFSRTIKENDYLNEKEYKLVINELKEKEKKIKLL LQAINLRPILELPQNSVGNLVSIFSRTIKENDYLNSERFKLINDELKEKEKOKIKNL SREKLTYVAQMEEVVSDLFFDIDAYLSDSWCRFPFYDVDFGWGKPIWVCLF OPYIKNUVVMMDYFFGDDYGIENJSEKMSAFEKNEQLLQFVSN"

244 C 252 g 415 t
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ANSORVSVSADPAKTIREALSKVLVYYPPFAGRIRWTENGDLEVECTGEGAVFVEAMA
DNDLSVLODFNEYDSFFOOLVFNLREDVNIEDLHLITVOVTRFTGGGFVVGTRFHFSV
SDGKGTGÓLLKGWGENRRESKERSLEPIWNREMVKPEDIMYLOFDHFDFINLER
SIQASWYISFERINYTKRCWMEEKREFSAFEVVVALIWLARTKSFRIPPNEYVKIIF
FIDMRNESFSDSPLEKGYYGANGGAMDNVKDLLNGSLLYALMLIKKSKFALNENFKS
RILTRFSTLDAMMHENVVGGGDWRNIGFYEDDFGGGGNAVNVSPMQOOREHELAMQNY
FLFLRSAKNMIDGIKILMFMPASMYKPFKIEMEVTINKYVAKICNSKL
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Direct Submission
Submitted (20-AUG-2000) Institute of Biological Chemistry,
Washington State University, PO Box 646340, Pullman, WA 99164-6340,
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Coniferopsida; Coniferales; Taxaceae; Taxus.
In (beservation) (1988)
Walker, K. and Croteau, R.
Taxol biosynthesis: Molecular cloning of a benzoyl- COA:taxane
2alpha -O-benzoyltransferase cDNA from Taxus and functional
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Taxus cuspidata 2-debenzoyl-7,13-diacetylbaccatin III-2-0-benzoyl
transferase mRNA, complete cds.
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Proc. Natl. Acad. Sci. U.S.A. 97 (25), 13591-13596 (2000)
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III-2-0-benzoyl transferase"
/protein.id="AAG38049.1"
/db_xref="GI:11559716"
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Pred. No. 8.8e+02;
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/db_xref="taxon:99806"
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Matches 13; Conservative
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RESULT 10 AF190130

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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE PUBMED

TITLE

FEATURES

AUTHORS REFERENCE

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/translation="MDLOTTCPIIKPSSPTPOHOSTYKLSIIDQLTPNVYFSIILLV
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ACLIKINDLDDLEQLLPPRHEGEPSDRSNLTVOVNYFGCEGMAIGLCFRHVIDATTA
AFTASLQETRASFERRPTREVVSAVILGALITATRESDDESNVPERLDTIISVNLRQ
RNNPPPFHOMGNIISGCLVYWPLEKKVDYGCLAKEIHESIKKVDDQFARKFYFDG
INLIPRIAGAEDVKRREFWYTSWCKTPLYEADFGMGNPKWAGNSMRLNQITVFFDSSDG
EGVERWYGLPRKAMPTSWCKTPLYEADFGMGNPKWAGNSMRLNQITVFFDSSDG
EGVERWYGLPRKAMPTSWCATPLYSPNPSIF"
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Fruit flavour related genes and use thereof
Patent: WO 0032789-A 44 08-JUN-2000;
AHARONI ASAPH (IL); VERHOEVEN HARRIE ADRIANUS (NL); LUECKER JOOST
(NL); CPRO DLO (NL); CONNELL ANN PATRICIA O (NL); TUNEN ARJEN
                                                                                                      Tunen, A.J.
Fruit flavour related genes and use thereof
Patent: WO 0032789-A 38 08-JUN-2000;
AHARONI ASAPH (IL); VERHOEVEN HARRIE ADRIANUS (NL); LUECKER JOOST
(NL); CPRO DLO (NL); CONNELL ANN PATRICIA O (NL); TUNEN ARJEN
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 1436)
Aharoni,A., Verkoeven,H.A., Luecker,J., O'Connell,A.P. and Van
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Aharoni,A., Verhoeven,H.A., Luecker,J., O'Connell,A.P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1436;
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Codon_start=1

/protein_id="CAC09068.1"

/db_xref="G1:10187189"
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Pred. No. 8.8e+02;
2; Mismatches 2;
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Sequence 44 from Fatent WO0032789.
AX025518
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/codon_start=1
/protein_id="CAC09065.1"
/db_xref="GI:10187183"
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/organism="Citrus limon"
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34. .1314
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/db_xref="taxon:3656"
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Location/Qualiflers
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76.5%;
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                                                                                                                                                                                                                                                                                                                                      /note="cDNA
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Best Local Similarity 76.5
Matches 13; Conservative
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JOHANNES VAN (NL)
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KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Coniferopsida; Coniferales; Taxaceae; Taxus.

1 (bases 1 to 1419)

Walker,K., Schoendorf,A. and Croteau,R.

Molecular cloning of a taxa-4(20),11(12)-dien-5alpha-ol-0-acetyl

Excherichia coli
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                                                                                                                                                                  Taxus cuspidata taxadienol acetyl transferase (TAT) mRNA, complete
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Walker, K., Schoendorf, A. and Croteau, R.
Direct Submission
Submitted (24-SEP-1999) Institute of Biological Chemistry, PO 646340, Pullman, WA 99164-6340, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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/protein_ld="AAF34254.1"
/db_xref="G1:6978038"
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Pred. No. 8.8e+02;
2; Mismatches 2;
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/organism="Taxus cuspidata"
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Sequence 38 from Patent WO0032789.
AX025512.
AX025512.1 GI:10187182
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76.5%;
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11. 1330
/gene="TAT"
                       1120 GATTTTGGATGGGGAAA 1136
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Best Local Similarity 76.5
Matches 13; Conservative
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

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BASE COUNT ORIGIN

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1 GAYTTYGGNTGGGGNAA 17
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               DADVSLEEFWDTLPYSLSSMQNNITHNALNSDEVLNSPLLLIQVTRLKCGGFIFGLCF
NHTMADGFGTVQFWKATAELRRGAFASTLPWQRALLTARDPPRITFRHYEYDQVVD
NHTWADGFGTVQFBARTAELRRGAFASTLPWQRALLTARDPPRITFRHYEYDQVVD
NHTWASGLIPVNKSTLOQFFFFTSQLQTSTRYDTLARTTAACFFF
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ITRGLVSFCVPFMNRNGEKGTALSLCLPPPAMERFRANNVHASLQVKQVVDAVDSHMQT
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HTVSDAPSELAFITAMSSMSKHIENDEDEERSKLEVPORSYIKYPTKEDSIYWRNA
LKFPLQSRHPSLPTPATGSKIKKLKGWIGSRVPSLVHLSSFVALDSYWMAG
ITKSFTADEDQDNEDAFFLIPVDLRPRLDPPVPENYFGRCLSYALPRMRRRELVGEKG
VRAARVIAABIKKRINDKRILETVEKWSPEIRKALCKSYFSVAGSSKLDLYGADFGW
GKRRKQEILSIDGEKYAMTLKARDFEGGLEVCLSLPKDKMDAFAAFSLGING"
31 5 C 131 9 411 L
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/protein_id="BAA93475.1"
/botein_id="C1:7415646"
/db_xref="C1:7415646"
/translation="VETCRYOPPPDSVAEQSVPLTFFDMTWLHFHPMLOLLFYEFPC
SKQHFSESIVPKLKQSLSKTLIHFFPLSCNLIYPSSPEKMPEFRYLSGDSVSFTIAES
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NIYPHNPSLEGRDPVKVIKEAIGKALVFYYPLAGRLREGPGRKLFVECTGEGILFIEA
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Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Saferidae; euasterids I; Lamiales; Lamiaceae; Perilla.
1 (sites)
Sakakibara,K.Y., Tanaka,Y., Mizutani,M.F., Fujiwara,H., Fukul,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB029340 1476 bp mRNA PLN 04-APR-2000 Perilla frutescens mRNA for anthocyanin acyltransferase, partial
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                                                                                                                                                                                                                                              Score 14.2; DB 9; Length 1471; Pred. No. 8.7e+02; 2; Mismatches 2; Indels 0;
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Molecular and biochemical characterization of a novel
hydroxycinnamoyl-CoA: anthocyanin 3-0-glucoside-6
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76.5%; Pred. No. 8.7e+02;
11ve 2; Mismatches 2;
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/db_xref="taxon:48386"
/tissue_type="leaf"
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2 (bases 1 to 1476)
Sakakibara,K.Y. and Tanaka,Y.
Direct Submission
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Best Local Similarity 76.5%;
Matches 13; Conservative
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TITLE
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Gaps

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C12R1:865),
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                                                                                                                        24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
MASAHIRO,
                                                                                                                                                                                                                                                                                 1 (bases 1 to 1479)
Ashikari, T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura, K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unidentified
unclassified.
1 (bases 1 to 1508)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T..
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                                                                                                       E12756 1479 bp DNA PAT 24-JU
Perilla ocimoides mRNA for acyltransferase,partial cds.
E12756
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    1. .1343 / product='acyltransferase'
    Location/Qualifiers

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ilarity 76.5%; Pred. No. 8.7e+02;
Conservative 2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                 Patent: JP 1997070290-A 4 18-MAR-1997;
SUNTORY LTD
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/organism="unidentified"
/db_xref="taxon:32644"
a 316 c 331 g 41:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strandedness: Double;
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JP 1997070290-A/4
18-MAR-1997
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1167 GATTTTGGATGGGGGAA 1183
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GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PALENT: JP 1997070290-A 5 18-MAR-1997;
SUNTONY LID
SUNTON DE 1997070290-A/5
PD 18-MAR-1996 JP 1996046534
PF 30-JAN-1996 JP 1996046534
PF 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 196915 PI
ASHIRARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI NAKAO
PI PUKUI, YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI JAKAAKI PC
                                                                                                                                                                                                                                                                                                      I FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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C12R1:865), PC (C12N9/10, C12R1:19); CC strandedness: Double; CC topology: Linear; FH Key Location FT source 1. .150E FT /C15sue_FT /C15sue_FT CDS 1. .1367 FT CDS 1. .1367
         TITLE
JOURNAL
                                                                                               COMMENT
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1. .1508 /organism='Senecto cruentus' /tissue_type='petal' /clone='pcAT48' /product='acyltransferase'. FEATURES

477 1. 1508 /organism="unidentified" /db_xref="taxon:32644" a 293 c 296 g 477 BASE COUNT ORIGIN

; 0 Query Match
Best Local Similarity 76.5%; Pred. No. 8.7e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0;

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Gaps

Db 1182 GATTTGGGTGGGGGAA 1198 1 GAYTTYGGNTGGGGNAA 17 õ

Search completed: November 5, 2001, 16:58:20 Job time: 11270 sec

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Anther specific control Aromatic acyl tran Aromatic acyl tran Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis anther specific gerobacco Antil

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AAC46170

Human gene express Human gene signatu Human prostate can Human secreted pro Human secreted pro Human colon cancer

us-08-894-356c-22.rng

Run on:

Title:

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Degenerate primer for identifying aromatic acyl transferase sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aromatic acyl transferase: transformation; anthocyanin pigment; plants; acylation; colour: tone; colouration; colour change; gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ss.
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95JP-0067159.
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AAT37314 standard; DNA; 17
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17-FEB-1995;
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                            Synthetic
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 RESULT
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Clone pTOM36. Lyc
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23.961 Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                hits satisfying chosen parameters:
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AAQ46682
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AAC49764
AAC39128
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Result No.

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ALIGNMENTS

Strawberry vesca a Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Clarkia breweri be

Neisseria meningit Arabidopsis thaila Neisseria meningit

AAA01753 AAZ53471 AAC46852

AAZ80421 AAX30844

AAF15736 AAC01828 Streptococcus pneu Human colon cancer Strawberry alcohol Strawberry alcohol Lemon acyl transfe Clarkia concinna b Clarkia concinna b Streptococcus pneu N. meningitidis pa

AAZ12045 AAC64780 AAC64780 AAC33536 AAC42254 AAC42254 AAC4766 AAC4785 AAC6478 AAC6478 AAC6428 AAC6428 AAC6428

a

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Query Match 83.5%;
Best Local Similarity 76.5%;
Matches 13; Conservative
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Best Local Similarity 76.5
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding geranylgeranyl diphosphate is useful for producing paclitaxel and other diterpenes that are useful as anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geranylgeranyl diphosphate synthase; GGPP synthase; yew; cytostatic; anticancer; Taxus; diterpene; paclitaxel; identification; plant; Taxomyces andreanae; Penicillium raistrickii; microorganism;
                                                                                                                                                                                                                                                                                                                    with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin planents. The arcmatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six
                                                                                                                                                                       plants
tone,
                                                                                                                                                                                                                                                                                                                                                                               tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAM37308-T37313. This degenerate primer was synthesised base on a peptide fragment (AAM04728) isolated from three of the six clones. It was used to identify
                                                                                                                                                                                                                                                                                              Vectors containing DNA fragments encoding proteins of plant origin
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                                                                                                                                                                  coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.5%; Score 14.2; DB 17; Length 17;
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                                                               Mizutani M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other aromatic acyl transferase encoding clones.
                                                         I, Fujiwara H, Fukui Y, Kusumi T,
Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 3 A; 0 C; 7 G; 3 T; 4 other;
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                                                                                                                                                                                                                                                    Claim 3; Page 82; 94pp; Japanese.
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100.08; FAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-282526/24.
                      (SUNR ) SUNTORY LID.
                                                                                                                         WPI; 1996-393401/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taxus canadensis.
                                                                                                                                                                                                          e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6043072-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2000
                                                                                   Nakao M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA13989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drugs
                                                                                                                                                                                           which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA13989/c
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The present sequence represents a PCR primer for a geranylgeranyl action diphosphate (GGPP) synthase protein. GGPP synthase has cytostatic activity. A vector encoding GGPP synthase is useful in increasing GGPP synthase levels in a host cell preferably Taxus (Yew) cell and thereby facilitates production, isolation and purification of larger amounts of GGPP synthase is useful in obtaining expression or enhanced expression of GGPP and other diterpenes, such as paciltaxel, useful as anticancer drugs. Isolated nucleic acids encoding GGPP synthase encoding nucleic acids are used for identifying genes encoding GGPP synthase from microorganisms such as Taxomyces andreanae and Penicillium raistrickii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is contained in a DNA construct used to transform host plant cells for regulating the prodn. of the enzyme encoded by pTOM36. Plants such as apple, tomato and mango may be modified to produce e.g. sweeter fruit, novel flavour, modified colour or to have improved processing characteristics. The DNA construct pref. also comprises a constitutive or regulatory promoter, e.g. the CaMV 35S or poly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.2; DB 12;
Pred. No. 74;
2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23 BP; 6 A; 9 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ray JA, Schuch WW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ11802 standard; DNA; 1080 BP
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76.5%;
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AAQ46682;

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Nucleotide sequence of the fiber protein encoded by adenovirus Ad-36p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the nucleotide sequence encoding the adenovirus Ad-36p fiber protein used in the method of the invention to determine if a person is suffering viral obesity. The method is used to determine whether obesity in a person has a viral basis, Ad-36p can be used as a basis of a vaccine to prevent viral-based obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining if obesity in a person is caused by Ad-36 virus - and providing the basis for treatment or prevention of obesity-causing, cholesterol reducing adenovirus, using the purified variant, Ad-36p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                  Adenovirus; Ad-36p fiber protein; viral obesity; vaccine; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1096 BP; 353 A; 215 C; 227 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 62347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
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                                                                                                                                         /*tag= a
/product= "Ad-36p fiber protein"
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Pred. No. 74;
2; Mismatches
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                                                                                                 Location/Qualifiers
1..1096
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76.5%;
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99US-01231E0.
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Best Local Similarity 76.5
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                                                                                                                                                                                                                                                                                                                                    (OBET-) OBETECH LLC.
                                                                     Mastadenovirus
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05-MAR-1999;
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                                                                                                        Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of the CDNA clone pTOM36 which is believed to encode a cytoplasmic protein of approximately 52000 daltons involved in the ribening of tomatces. The clone is 1069 bases long with an open reading frame of 271 codons. DNA homologous to pTOM36 may be used in a construct that inhibits expression of genes homologous to pTOM36 during ripening. Fruit from plants transformed with this construct have increased solids content and a higher content of reducing sugars, e.g. glucose and fructose. The fruit may be mangoes, peaches, apples, pears, strawberries, bananas, melons and esp. tomatoes, which are useful in the prodn. of
                                                                                                                                                                                                                                                              Transgenic fruit production; prodn.; increased solids content; higher reducing sugar content; tomato; tomatoes; plant cultivation; improved; paste; soup; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic fruit with increased solids content - is obtd. by cultivating plants, esp. tomatoes, in which expression of genes homologous to prOM36 is inhibited
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.5%; Score 14.2; DB 14; 76.5%; Pred. No. 74;
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                                                                                                                     AAQ46682 standard; cDNA; 1080 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            improved tomato paste and soup.
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1 GAYTTYGGNTGGGGNAA 17
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Matches 13; Conservative
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                                                                                                                                                                                                                             pTOM36 cDNA clone
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07 - JUL - 1999
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99 - JUL - 1999
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15-JUL-1999;
16-JUL-1999;
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19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
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13-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO: 4961.
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.2; DE
Pred. No. 76;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC33965 standard; DNA; 1429 BP
990S-0157865.
990S-0158029.
990S-0158039.
990S-0158039.
990S-0159293.
990S-0159293.
990S-0159330.
990S-0159330.
990S-0159637.
990S-0159637.
990S-0160767.
990S-0160989.
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990S-012548.
990S-0125788.
990S-0126264.
990S-0126785.
990S-01267824.
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76.5%;
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1161 gatttcggttggggtaa 1177
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nes 13; Conservative
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05-MAR-1999;
03-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
06-0CT-1999,
07-0CT-1999,
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Best Local S1
Matches 13;
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99US-0159329

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990S-0144335.
990S-0144632.
990S-0144884.
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990S-0145086.
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99US-0148341.
99US-0148565.
99US-0148684.
99US-0149368.
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99US-0147192.
99US-0147260.
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99US-0147935.
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99US-0149929.
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99US-0151065
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12-0CT-1999;
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13-0CT-1999;
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04-OCT-1999
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Pred. No. 76;
2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                        AAC64784 standard; cDNA; 1436 BP.
                                      9905-0159584
9905-0159584
9905-0160741-
9905-0160767-
9905-0160770-
9905-0160815-
9905-0160815-
9905-0160981-
9905-0161404-
9905-0161405-
9905-0161405-
9905-0161359-
9905-0161359-
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76.5%;
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99US-0161993
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les 13; Conservative
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Matches
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us-08-894-356c-22.rng

08-JUN-2000

alcohol acyl transferase, alcohol dehydrogenase, pyruvate decarboxylase, aminotransferase and esterase activities, which are involved in the biosynthetic pathway for allohal dehydrogenase, pyruvate decarboxylase, aminotransferase and esterase activities, which are involved in the biosynthetic pathway for allohalts and/or aromatic ester production in fruit. The nuclectide sequences can be inserted into the genome of a fruit-producing plant to regulate aliphatic and/or aromatic ester formation. Aromatic and/or aliphatic esters in microorganisms, plant cansferase are produced by inserting thiolase, alcohol acyl ransferase and esterase nuclectide sequences into the genome and feeding the microorganism or plant with alcohol, aldehydes, alpha-keto acids, or amino acids and fatty acids, and acyl-CoA. The nuclectides and their proteins can be used in the processed food industry as food additives to enhance the flavour of syrups, ice-creams, frozen desserts, yoghurts and confectionery. They are used: as flavouring agents for oral medications and vitamins; provide flavour and aroma in beverages, including alcohol; enhance or reduce fruit flavour, aroma, fragrance or scent; enhance the flavour or aroma of natural, synthetic or artificial ground and accompances; as antifactal or antifundant alcohol; and or antificial flavour, and subjects as antifactal or antifundant accompances. perfumes in cosmetics, creams, sun-protectant products, hair conditioners, lengthening agents and fixatives in perfumes, suspension aids for aluminium salts in anti-perspirant pharmaceuticals, cleaning products, personal care products and animal care products; as disinfectant additives; as degreasing solvents for electronics; as miticides, scabicides, plasticisers and decdorants. The present sequence encodes lemon alcohol acyl transferase, from the present invention. A new DNA sequence encoding a polypeptide with alcohol acyl transferase activity for producing and regulating aromatic and/or aliphatic ester formation in microorganisms, plant cells or plants present invention describes nucleotide sequences with thiolase, Score 14.2; DB 21; Length 1436; Example 5; Page 114-115; 163pp; English. 6 12:43:00 2001 83.5%; 76.5%; 1 GAYTTYGGNTGGGGNAA 17 13; Conservative Query Match Best Local Similarity Thu Dec 6 Matches AAC64787 q ô

Sequence 1436 BP; 410 A; 280 C; 320 G; 426 T; 0 other;

Indels ; ; 2; Mismatches Pred. No. 76; AAC64787 standard; cDNA; 1470 BP

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Gaps

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Strawberry; fruit flavour; biosynthetic pathway; aliphatic; thiolase; aromatic ester; alcohol acyl transferase; alcohol dehydrogenase; pyruvate decarboxylase; aminotransferase; esterase; alcohol; aldehyde; alpha-keto acid; amino acid; fatty acid; acyl-CoA; processed food; food additive; flavour; syrup; ice-cream; frozen dessert; yoghur; confectionery; flavouring; oral medication; vitamin; aroma; beverage; alcohol; scent; fragrance; perfume; cosmetic; suspension aid; aluminium salt; anti-perspirant; pharmaceutical; cleaning product; insect pheromone; dye cartiers; solvent; insect repellent; miticide; scabicide; plasticiser; deodorant; ss. Honey dew melon alcohol acyl transferase encoding cDNA SEQ ID NO:23A. 28-FEB-2001 (first entry) Cucumis sp. AAC64787;

WO200032789-A1

The present invention describes nucleotide sequences with thiolase, alcohol acyl transferase, alcohol dehydrogenase, pyruvate decarboxylase, alcohol acyl transferase, alcohol dehydrogenase, pyruvate decarboxylase, anicohortansferase and esterase activities, which are involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit. The nucleotide sequences can be inserted into the genome of a fruit. The nucleotide sequences can be inserted into the genome of a formation. Aromatic and/or aliphatic esters in microorganism, plant cells or plants are produced by inserting thiolase, alcohol acyl minotransferase, alcohol dehydrogenase, pyruvate decarboxylase, aninotransferase and esterase nucleotide sequences into the genome and feeding the microorganism or plant with alcohol, aldehydes, alpha-keto aciditives to enhance the flavour of syrups, ice-creams, frozen desserts, cadditives to enhance the flavour of syrups, lee-creams, frozen desserts, or additives to enhance the flavour of syrups, lee-creams, frozen desserts, including alcohol; enhance or reduce fruit flavour, aroma, fragrance or scent; enhance the flavour or aroma of natural, synthetic or artificial products; for the production of novel combinations of artificial geness as antibacterial or anti-fungal agents; as fragrance or perfumes in cosmetics, creams, sun-protectant products, as as suspension and storal aluminum salts in anti-fungal agents in perfumes, suspension and along and animal care products, as a series of a products. insect pheromones; and as dye carriers, solvents, insect repellents, mitloides, scabicides, plasticisers and deodorants. The present sequence encodes honey dew melon alcohol acyl transferase, from the present A new DNA sequence encoding a polypeptide with alcohol acyl transferase activity for producing and regulating aromatic and/or aliphatic ester formation in microorganisms, plant cells or plants O'Connell AP; disinfectant additives; as degreasing solvents for electronics; as Verhoeven HA, Van Tunen AJ, (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD Example 5; Page 121-122; 163pp; English. 99WO-NL00737. 98EP-0204018 99EP-0200739 Aharoni A, Luecker J, WPI; 2000-412335/35 P-PSDB; AAB36461 02-DEC-1999; 02-DEC-1998; 12-MAR-1999; invention. activity

Sequence 1470 BP; 415 A; 301 C; 334 G; 420 T; 0 other;

Gaps ö 83.5%; Score 14.2; DB 21; Length 1470; 76.5%; Pred. No. 77; Live 2; Mismatches 2; Indels 0; 13; Conservative Query Match Best Local Similarity Matches

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AAC39128 standard; DNA; 1477 BP. RESULT 10 AAC39128 qq

1 GAYTTYGGNTGGGGNAA 17

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Arabidopsis thaliana DNA fragment SEQ ID NO: 23476. 17-OCT-2000 (first entry)

AAC39128;

Hybridisation assay; genetic mapping; gene expression control;

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99US-0140695

24 - JUN - 1999; 28 - JUN - 1999; 29 - JUN - 1999; 30 - JUL - 1999; 01 - JUL - 1999; 02 - JUL - 1999; 06 - JUL - 1999;

08-JUL-1999; 09-JUL-1999; 12-JUL-1999; 13-JUL-1999;

14 - 70L - 1999; 15 - 70L - 1999; 16 - 70L - 1999; 19 - 70L - 1999; 20 - 70L - 1999;

20-JUL-1999; 20-JUL-1999; 21-JUL-1999;

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metabolic pathway; promoter; termination sequence; ss
protein identification; signal transduction pathway;
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990S-0139461.
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990S-0139750.
990S-0139763.
990S-0139817.
990S-0140353.
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                                               Arabidopsis thaliana
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03-AUG-1999 04-AUG-1999 99US-0151438 99US-0151930

31-AUG-1999 01-SEP-1999

09-AUG-1999 110-AUG-1999 110-AUG-1999 113-AUG-1999 113-AUG-1999 114-AUG-1999 118-AUG-1999 σ

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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferaes activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                         which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylatton; colour; tone; colouration; colour change; Gentiana triflora; Petunia, hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.2; DB 17; Length 1479; Pred. No. 77; 2; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                   - for transforming
                                                                                                                                                                     Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1479 BP; 420 A; 316 C; 331 G; 411 T; 1 other;
3..1343
/*tag= a
/product= Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product- Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                   coding for aromatic acyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT37312 standard; cDNA to mRNA; 1508 BP
                                                                                                                                                                                                                                                                           Claim 4; Page 65-69; 94pp: Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Senecio cruentus (Clone pGAT8).
                                                                                                                                                                               Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                              83.5%;
76.5%;
                                                                                                      96JP-0046534.
95JP-0067159.
95JP-0196915.
                                                                                    96WO-JP00348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.5
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3..1367
                                                                                                                                                 (SUNR ) SUNTORY LTD.
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                                                                                    16-FEB-1996;
                                           WO9625500-A1
                                                              22-AUG-1996.
                                                                                                       30-JAN-1996;
                                                                                                                            29-JUN-1995;
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                                                                                                                   17-FEB-1995
                                                                                                                                                                                 Nakao M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT37312;
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    cps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.2; DB 21;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT37311 standard; cDNA to mRNA; 1479 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perilla ocimoides (Clone pSAT208).
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         990S-0153070.
990S-0153758.
990S-0154018.
990S-0154039.
990S-0155139.
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76.58;
                                                                                                                                                                               59293.
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                                                                                                                                                                                                                                                                 99US-0159584
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99US-0161359
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1186 gatttcggttggggtaa 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
                                                                                 99US-015
99US-015
99US-015
                                                                                                                                                                              990S-01
990S-01
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Best Local Similarity
                                                                      23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT37311;
                                                                                                                                    06-0CT-19
                                                                                                                                                                                                                                                     14-0CT-19
18-0CT-19
                                                                                                                                                                                                                                            14-OCT-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Gaps

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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT31308-T37313. NOTE: This sequence is supposed to cross reference with the protein described in AAW04727, however there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide given in the specification and described in AAW04727 that the indexer decided not to cross reference the two.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA related with fruit ripening - can be used to genetically modify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "contains a putative polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canteloupe charentais; fruit ripening control; promoter; ss.
                                                                                                                                     DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin plyments and thus altering colour e.g. of flowers
                                             Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1518 BP; 384 A; 340 C; 366 G; 428 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Karvouni 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.2; I
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melon ripening-related cDNA clone MEL2.
                                             Fukul Y,
                                                                                                                                                                                                                                        Claim 4; Page 73-76; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1385..1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           John I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT89415 standard; cDNA; 1526 BP.
                                                                 Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.5%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||:||:|| ||||| ||
1176 gattttggatggggtaa 1192
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                                             Fujiwara H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greierson D,
  (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-503108/46.
                                                                                                          WPI; 1996-393401/39
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZENE ) ZENECA LTD.
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ethylene; MEL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cucumis melo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-APR-1998
                                             Ashikari T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aggelis A,
                                                                   Nakao M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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3'UTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                                                                                                DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vectors containing DNA fragments encoding proteins of plant origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana trifloza; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula anqustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.2; DB 17; Length 1508; Pred. No. 77;
                                                                                                                                                                                               Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1508 BP; 442 A; 294 C; 295 G; 477 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT37313 standard; cDNA to mRNA; 1518 BP.
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                                                                                                                                                                                           Asnıkarı T, Fujiwara H, Fukui Y,
Nakao M, Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 69-72; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 1..1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.5%;
76.5%;
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95JP-0067159.
95JP-0196915.
                      96WO-JP00348
                                                                                   95JP-0067159,
95JP-0196915,
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|1182 gattttgggtggggaa 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 76.5
Matches 13; Conservative
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P-PSDB; AAW04726.
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                    16-FEB-1996;
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                                                               30-JAN-1996;
                                                                                                          29-JUN-1995;
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29-JUN-1995;
                                                                                   17-FEB-1995;
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Indels

Length 1518;

DB 17; 5;

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                                                                      novel ripening-related product from Cucumis melo. It is one of two specified sequences (MEL2) 1526 bp or (MEL7) 686 bp which were 1solated from a melon ripe fruit cDNA library. MEL2 is not a full-length clone; it lacks the initiation codon for the amino terminus. The cDNA allows control of the ripening of fruit, especially melons.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anther specific cDNA or genomic sequences can be used to identify and isolate anther specific promoters. The anther specific promoter can then be cloned into a recombinant construct and used to express heterologous genes. Preferred heterologous genes include Diptheria toxin A-chain gene; pectate lyase gene pelE from Erwinia chrysanthemi; T-urfil from cms-T maize mitochondrial genomes; the Gin recombinase gene from phage Mu; the indole acetic acid-lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic plants; male sterility; pollen; sterile; seel febilination; seed; hybrid; toxin-A; pelE; T-urfil; Gin; iaal; CytA; toxin; Nicotiana tabacum; Diptheria; Ervinia chrysanthemi; phage Mu; Psuedomonas syringae; Bacillus thuringiensis; anther;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anther-specific cDNA, genomic and recombinant DNA - produce transgenic male-sterile plants, which prevents self-pollination,
                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                          Length 1526
                                                                                                                                                             Sequence 1526 BP; 439 A; 297 C; 331 G; 448 T; 2 U; 9 other;
                                                          This cDNA sequence is from the MEL2 clone which produces a
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                        83.5%; Score 14.2; DB 18; 76.5%; Pred. No. 77;
                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                     2; Mismatches
 especially melons to control ripening
                             Claim 1; Pages 18-19; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
66..1412
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 21-24; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anther specific cDNA clone ant32.
                                                                                                                                                                                                                                                                                                                                                                      AAQ54685 standard; cDNA; 1542 BP
                                                                                                                                                                                                                                                                                             1136 gactttggatggggaaa 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93EP-0810455
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                 1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                      Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuttle AB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in hybrid seed prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-010428/02.
P-PSDB; AAR47475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crossland LD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breeding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP578611-A
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                                                                                                                                                                                                        Query Match
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Gaps
synthetase gene from Pseudomonas syringae and the CytA toxin gene from Bacillus thuringiensis Israeliensis. All of these genes when expressed in anther tissue will result in the lability of the plant to produce viable pollen. Transformation of plants with such a recombinant construct can produce transgenic, male sterile plants. Male sterility is important in the production of hybrid seeds as it prevents self pollination which hinders breeding and hybrid seed
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                            Length 1542;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                 Sequence 1542 BP; 473 A: 293 C; 332 G; 444 T; 0 other;
                                                                                                                                                                                                                                                                                                         DB 15;
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                                                                                                                                                                                                                                                                                                       Score 14.2; DE Pred. No. 77; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5, 2001, 18:12:09
                                                                                                                                                                                                                                                                                                       83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAYTTYGGNTGGGGNAA 1.7
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: November
Job time: 15464 sec
                                                                                                                                                                                production.
                                                                                                                                                                                                                                                                                                            Query Match
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US-07-598-873-1
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Matches
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q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 74, Appli
Sequence 24, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                               ; Search time 168.74 Seconds
(without alignments)
19.072 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-187-050-6
US-07-598-873-1
US-08-396-531-1
US-08-396-531-1
US-09-125-11
US-09-125-11
US-08-207-904-16
US-08-207-904-16
US-08-207-904-16
US-08-207-904-16
US-08-207-904-16
US-08-207-904-16
US-08-127-108-5
US-08-472-188-74
US-08-472-188-74
US-08-472-188-74
US-08-412-1844-24
US-08-112-1844-24
US-08-112-184-24
US-08-112-184-24
US-08-112-184-24
US-08-112-184-24
US-08-112-184-24
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US-08-112-184-24
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US-08-1
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US-07-695-472B-35
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US-07-695-472B-36
US-07-916-098A-44
                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-250-740-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-695-472B-1
                                                                                                                                                                                                                                                                                                          324599 segs, 94655562 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                 November 5, 2001, 18:05:10
                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                                                 - nucleic search, using sw model
                                                                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                     1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
                                                                                                                                                                            US-08-894-356C-22
                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match
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                                                                                                                                                                                                                                                        Scoring table:
                                                                                 OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                      Seguence:
                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                      Title:
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US-09-187-050-6/C

Sequence 6, Application US/U9187050B

Sequence 6, Application US/U9187050B

Sequence 6, Application US/U9187050B

PAPLICANT: Croteau, Rodney B

APPLICANT: Hefner, Jerry

TITLE OF INVEWINON: Synthase, And Methods of Use

TITLE OF INVEWINON: Synthase, And Methods of Use

TITLE NEW PERENCE: WSUB1243

CURRENT APPLICATION NUMBER: US/09/187,050B

CURRENT FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6

LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                             Sequence 1, Appl1
Sequence 5, Appl1
Sequence 35, Appl
Sequence 36, Appl
Sequence 1, Appl1
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 150, Appl
Sequence 150, Appl
Sequence 150, Appl
                                                                                                                                                                          Sequence 150, App
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Sequence 1, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: Description of Artificial Sequence: non-degenerate OTHER INFORMATION: reverse PCR primer
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 23;
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Patent No. 5254800

GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: GRIERSON, DONALD
APPLICANT: SCHUCH, WOLEGANG W
TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS;
TITLE OF INVENTION: DERIVED THEREFROM
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KET: misc_difference
LOCATION: (1)..(23)
CTHER INFERMATION: No. 6043072-degenerate PCR primer
US-09-187-050-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
m
           US-08-295-502-1

US-08-295-502-1

US-08-519-547A-5

US-07-695-472B-4

US-07-49-446-1

US-07-749-446-1

US-07-749-646-1

US-07-749-646-1

US-08-149-101A-5

PCT-US94-1283-5

US-08-906-616-150

US-08-906-616-150

US-08-906-614-150

US-09-012-692-150

US-09-012-692-150

US-09-012-692-150

US-09-012-692-150

US-09-012-692-150

US-09-012-692-160

US-09-012-692-160

US-09-012-692-160

US-09-012-692-160

US-09-012-692-160

US-09-012-692-160

US-09-012-692-160

US-09-012-692-160
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76.5%; Pred. No. 8.4;
ilve 2; Mismatches
                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 GATTTCGGCTGGGGTAA 4
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nes 13; Conserv
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Patent No. 5744364

GENERAL INFORMATION

APPLICANT: BIRBD, COLIN R

APPLICANT: RAY, JOHN A

APPLICANT: SAUCH, WOLEGANG W

TITLE OF INVENTION: DRAY, CONSTRUCTS, CELLS AND PLANTS

TITLE OF INVENTION: DRAY, CONSTRUCTS, CELLS AND PLANTS

TITLE OF SEQUENCES: 5

CORRESPONDENCE ADDRESS: 5

ADDRESSEE: CUSHMAN, DARRY & CUSHMAN

ADDRESSEE: CUSHMAN, DARRY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: Ninth Floor, 1100 New York Avenue, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,531
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Lycopersicon esculentum
STRAIN: Ailsa Craig
DEVELOPMENTAL STAGE: Ripening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,037
FILING DATE: 16-ARR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELERA: 202-861-3004
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERIFICS:
LENGTH: 1080 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: KOKULIS, PRUL N.
REGESTRATION NUMBER: 16,773
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPK: 202-861-300
TELEK: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1080 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:||:|| ||||| ||
866 GATTTTGGATGGGGAAA 882
                         NAME: DEAVER, DONALD B REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 13; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-073-425-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-08-396-531-1
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COUNTRY: USA

ZIP: 2005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,425
FILING DATE: 09-UNN-1993
''ASSIFICATION: 800
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/598,873
FILING DATE: 19991019
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-300
TELEFA: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SECUENCE CRARACTERISTICS:
LENGTH: 1080 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: double
TOPOLOGY: linear
3: CUSHMAN, DARBY & CUSHMAN
Eleventh Floor, 1615 L Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.2; DE Pred. No. 14; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BONINELL, JEREMY M.
APPLICANT: BONINELL, JEREMY M.
APPLICANT: GRIERSON, DONALD
APPLICANT: RAY, JOHN A
APPLICANT: ROUCH, WOLFGANG W
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARRY & CUSHMAN
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08073425
Patent No. 5569829
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: Ailsa Craig
DEVELOPMENTAL STAGE: Ripening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAYTTYGGNTGGGGNAA 17
||:||:|| || || ||
866 GATTTTGGATGGGGAAA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 76.5
Marches 13; Conservative
                                           Washington
                                                                                          COUNTRY: USA
ZIP: 20036-5601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
  ADDRESSEE:
                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-073-425-1
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Gaps

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APPLICANT: Tuttle, AnnMarie
APPLICANT: Tuttle, Lyle D.
TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                    Length 1512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-100S/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREW APPLICATION NATA:
APPLICATION NUMBER: US/08/207,904
                                      DB 3;
                                    Score 14.2; DE
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.5%; Score 14.2; I
76.5%; Pred. No. 15;
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/908,242
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REGISTRATION NUMBER: GG 1624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                           CIBA-GEIGY Corporation
                                                                                                                                                                                                      RESULT 7
US-08-207-904-1
; Sequence 1, Application US/08207904
; Patent No. 5477002
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (919)541-8615
TELEFAX: (919)541-8699
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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| 1239 GATTTTGGGTGGGGAAA 1255
                                                                                                                                    7 Skyline Drive
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                                                                                                              1 GAYTTYGGNTGGGGNAA 17
                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Nicotiana INDIVIDUAL ISOLATE:
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                                      Query Match
Best Local Similarity
Matches 13; Conserv
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CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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; LOCATION:
US-08-207-904-1
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                                                                                                                                                                                                            Length 1080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Atkinson, Richard L.
APPLICANT: Atkinson, Richard L.
APPLICANT: Dhurandhar, Nikhil V.
TITLE OF INVENTION: Viral Obesity Methods and Compositions
FILE REFERENCE: 710395, 90010
CURRENT APPLICATION NUMBER: US/09/056,153
CURRENT APPLICATION NUMBER: US/09/056,153
SOFTWARE: 1998-04-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.
LENGTH: 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                          Score 14.2; DB 1;
Pred. No. 14;
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Pred. No. 14;
2; Mismatches
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APPLICANT: Aggelis, Alexandros

APPLICANT: Gererson, Donald

APPLICANT: Gererson, Donald

APPLICANT: Gererson, Donald

TILE OF INVENTION: Fruit Ripening

TILE REFERENCE: SEE5011/UST

CURRENT APPLICATION NUMBER: US/09/142,514A

CURRENT APPLICATION NUMBER: PCT/GB97/00824

EARLIER APPLICATION NUMBER: GB 9606906.7

EARLIER FILING DATE: 1997-03-24

EARLIER FILING DATE: 1996-04-02

SOFTWARE: PALENTING NOS: 4

SOFTWARE: PALENTIN NOS: 4
                                                                                                                                                                                                                                                   2; Mismatches
                                                                            , OKGANISM: Lycopersicon esculentum; STRAIN: Ailsa Craig; DEVELOPMENTAL STAGE: Ripening US-08-396-531-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09142514A Patent No. 6107548
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09056153 Patent No. 6127113
              TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                            83.5%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Adenovirus type 36P
US-09-056-153-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.5%;
76.5%;
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                       1 GAYTTYGGNTGGGGNAA 17
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Best Local Similarity 76.5
Matches 13; Conservative
STRANDEDNESS: double
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COCANISM: Cucumis melo
US-09-142-514-1
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Gaps

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APPLICANT: Harrison, David G.
APPLICANT: Alexander, R. Wayne
APPLICANT: MITPHY, T.J.
APPLICANT: Mishida, Wen'ichi
TITLE OF INVENTION: Endothelial Nitric Oxide Synthase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
                                             Sequence 1, Application US/07908245 Patent No. 5498539
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.
ZIP: 30309-4530
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Best Local Similarity
Matches 13; Conserv
                                                                                               GENERAL INFORMATION:
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ORIGINAL SOURCE:
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                          JS-07-908-245-1/c
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                                                                                                      APPLICANT: Tuttle, AnnMarie
APPLICANT: Tuttle, Lyle D.
TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
NUMBER OF SEQUENCES: 2.1
CORRESPONDENCE ADDRESS:
ADDRESSE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STREET: New York
COUNTRY: USA
ZIP: 10532
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US-08-207-904-16
                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Nicotiana tabacum
INDIVIDUAL ISOLATE: Ant32 genomic clone
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/908,242
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTARTION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CGC 1624
TELECOMMUNICATION INFORMATION:
TELEFAN: (919)541-8615
RESULT 8
US-08-207-904-16
Sequence 16, Application US/08207904
Patent No. 5477002
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.5%;
ilarity 76.5%;
Conservative
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2076..3422
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Best Local Similarity
Matches 13; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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LOCATION:
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US-09-123-708-5/C

Sequence 5, Application US/09123708

Sequence 5, Application US/09123708

Sequence 5, Application US/09123708

GENERAL INFORMATION:

APPLICANT: SCHRADER, Juergen

APPLICANT: GOBBOCKE, Axel

TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

FILE REFERENCE: 511169-2003

CURRENT APPLICATION UNMER: US/09/123,708

CURRENT FILING DATE: 1998-07-28

EARLIER APPLICATION NUMBER: 08/553,503
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              MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,245
FILING DATE: 19920702
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
REFERENCE/POCKET NUMBER: EWU 111
TELECOMMULCATION INFORMATION:
TELEPHONE: 404-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
85;
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Pred. No.
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76.5%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4089 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL TYPE: Endothelial US-07-908-245-1
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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3249 GATTTGGGTGGGGAAA 3265

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MICHIGAN
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                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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US-08-479-285-74
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APPLICANT: SCHRADER, Jurgen
APPLICANT: GOBECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2004
CURRENT APPLICATION NUMBER: US/09/123,624
CURRENT APPLICATION NUMBER: 08/553,503
PRIOR APPLICATION NUMBER: 08/553,503
PRIOR FILING DATE: 1994-03-01
PRIOR FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 5
LENGTH: 4097
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APPLICANT: MEZES, PETER S
APPLICANT: GOULLIE, BRIAN B
APPLICANT: ANDERSON, WH KERR
APPLICANT: ANDERSON, WH KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: MAPPLICANT
CORRESPONDENCE ADDRESS:
ADDRESSE: DUANE C ULMER
STREET: P.O. BOX 1967
CITY: MIDLAND
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85;
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Pred. No. 85;
1; Mismatches
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Pred. No. 85;
1; Mismatches
                EARLIER APPLICATION NUMBER: P4411402.8
EARLIER FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4097
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Patent No. 6149936
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EARLIER FILING DATE: 1996-03-01
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.5%;
Matches 13; Conservative
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                      TYPE: DNA
CYCOMEGALISM: Cytomegalovirus
US-09-123-708-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Bos taurus
US-09-123-624-5
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Sequence 74, Application US,08479285

Patent No. 6207815

GENERAL INFORMATION:

APPLICANT: MEZES, PETER S

APPLICANT: RIXON, MARK W

APPLICANT: RIXON, WARK W

APPLICANT: ROUGHSON, WH KERR

APPLICANT: SCHOLOM, JEFFREY

TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 508;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US.08/479,285 FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.6; DB 2;
Pred. No. 1.1e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                 NAME: ULMER, DUANE C
REGISTRATION NUMERS: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040687
FILING DATE: 31-MAR-19/3
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Gisk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.18;
70.68;
                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 508 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 70.6
Matches 12; Conservative
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P.O. BOX 1967
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1 GAYTTYGGNTGGGGNAA 17
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US-08-646-590B-24
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Patent No. 5814473
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: & BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                74.1%; Score 12.6; DB 4; Length 508; 70.6%; Pred. No. 1.1e+02; Live 2; Mismatches 3; Indels
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,171A
FILING DATE: CONCULTENTLY
               NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636 8104
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: HERROW, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 3314(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAN: 201-994-1744
ULMER, DUANE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: LINEAR MOLECULE TYPE: GENOMIC DNA
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 912 NUCLEOTIDES
                                                                                                                                             LENGTH: 508 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                            1 GAYTTYGGNTGGGGNAA 17
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STRANDEDNESS: SING
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Matches 12; Conserve
                                                                                                                                                                                                          linear
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US-08-599-171A-24
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US-08-479-285-74
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74.1%; Score 12.6; DB 1; Length 912; 70.6%; Pred. No. 1.2e+02; Live 2; Mismatches 3; Indels

Conservative

Query Match Best Local Similarity Matches 12; Conserva

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Sequence 24, Application US/08646590B
Fatent No. 5962283
GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Warnson, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.1%; Score 12.6; DB 2; 70.6%; Pred. No. 1.2e+02; Live 2; Mismatches 3;
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; LOCATION: 1...909
US-08-646-590B-24
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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Matches 12; Conserv
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em_estpl9:*
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                                                                                                                     ; Search time 5816.79 Seconds (without alignments) 27.627 Million cell updates/sec
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Contact: Shoemaker Rylublic Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fex: 314 286 1800
                                                                                                                        Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                      /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-c1004-7183" /clone_lib="Gm-c1004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.5%; Score 14.2; DB 21; Length 227; 76.5%; Pred. No. 1.2e+03; ive 2; Mismatches 2; Indels 0;
                                                                                                                                                                         Info@genomesystems.com web site: www.genomesystems.com
Insert Length: 489 Std Error: 0.00
Seq primer: -40RP from Gibco
Pobrya.No.
                                                                                                                                                                                                                                               /organism="Glycine max"
                                                                                                                                                                                                                                                                                       /tissue_type="root"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                            Location/Qualifiers
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BB264508 BB264508
AW471629 Sil3h01.y
AZ813888 ZM0081821
AQ034368 CIT-HSP-2
BE460581 EST412000
AL378020 MtBB35502
BG508347 SaC95e04.
AW350346 GM210009A
RG3665 y110f04.s1
AU967062 496021811
AU095989 AU095989
                                                                                                                                                                                                                                                                            AV407679 AV407679
BE213479 GF-FV-P6E
BG042849 saa45f04.
BE020415 sm43h12.y
AV539490 AV539490
                                                                                                                                                                                                                                                                                                                                                           W08160 mb42d05.r1
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AW318655 un03b01.y
BE461054 EST412473
AA394828 26611 Lam
AQ186186 HS 3074_B
BF009723 ss84002.y
BG442050 GA_Ea001
BG444080 GA_Ea002
AA713159 32719 Lam
BE432935 EST399380
A18399317 EST268660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW255739 ML800 pep
AW650512 EST328966
BF324543 su25c03.y
AI856260 sb39912.x
                                                                                         BG550470 947076G02
AZ015624 RPCI-23-2
AA650754 30868 Lam
BG046171 saa49e12.
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AI748527 sb54c08.y
AV425743 AV425743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glýcine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
1 (bases 1 to 227)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
                                                             AI494813 sa96g04.y
AW234169 sf22a08.y
                                                                                                                                    AA651035 31149 Lam
                                           Description
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            SUMMARIES
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BF009723
BG442050
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BE213479
                                                                                                                                                                                                                                      AW350546
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AI608251
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                                                                                           mRNA sequence.
AI494813
                                                                                                      soybean.
                                           Score
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Alcala, J. Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Arbi: cLED - Tomato Carpel EST Library .01godf-primed and directionally cloned cDNA in vector Lamda ZAP II with 5' and 3' ends located at the EcoR1 and Arbi sites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG550470 247 bp mRNA EST 09-APR-2001
947076G02.x2 947 - 2 week shoot from Barkan lab Zea mays CDNA, mRNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                             ESTA6768 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED21D13, mRNA sequence.
                                                                                       Length 244;
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1. .247
/organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                             DB 113;
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Pred. No. 1.2e+03;
                                                                                          Score 14.2; DB 11
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4366
Fax: 864 656 4293
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Clemson University
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/clone="cLED21D13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum
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76.5%;
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Best Local Similarity 76.5
Matches 13; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae: eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.

I (bases 1 to 244)

Shoemaker,R., Reim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,Public Soybean EST Project

Unpublished (1999)
                   AW234169 244 bp mRNA EST 17-JUL-2000 sf22a08.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-687 5' similar to TR:Q43583 Q43583 HSR201 PROTEIN. ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3225 FXX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com Insert Length: 486 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-687"
/clone_lib="Gm-c1028"
/lssue_type="roots of 'Supernod' plants"
/lab_host="DH108"
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Fax: 314 286 1810
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Gaps

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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 258)
Newman,T., deBrulin,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,E., Ohlrogge,J., Ralkhel,N., Somerville,S., Thomashow,M., Retzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Crgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially dispsted
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

3 6 6 1
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                     Dmail: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA650754 258 bp mRNA EST 31-OCT-1997
30868 Lambda-PRL2 Arabidopsis thaliana cDNA clone 281H6T7, mRNA
sequence.
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Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
Lansing,Ml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 249;
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Pred. No. 1.2e+03;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                              1. .249
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                  /strain-"C57BL/6J"
/db_xrei="taxon:10090"
/clone="RPCI-23-258D7"
/clone="lib="RPCI-23"
/sex="Female"
/lab_hogt="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7 dye primer.
Location/Qualifiers
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AA650754.1 GI:2580846
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76.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chao.S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-258D7.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
1 Institute for Genomic Research
1 131 Medical Center Dr., Rockville, MD 20850, USA
1 131 838 0200
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                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sepermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
1 (bases 1 to 247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 249)
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RPCI-23-258D7.TJ RPCI-23 Mus musculus genomic clone RPCI-23-258D7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: walbotestanford.edu
Plate: 94/706 row: G column: 02.
Location/qualifiers
1. 247
/organism="zea mays"
/cultivar="B13"
/db_xref="taxon:4577"
/clone_lib="947 - 2 week shoot from Barkan lab"
/tissue_type="leaf and stem, including leaf base"
/dev_stage="z week old seedling (3 leaves)"
/lab_host="XL1-Blue"
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                                                                                                                                                                                                                                                  University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 725 8221
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76.5%;
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Best Local Similarity 76.5
Matches 13; Conservative
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                                                                    Zea mays.
Zea mays
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GACTTTGGTTGGGGGAA 105
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritterten, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                   /note-Tvector: lambda Z1p-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and saliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: estewatson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG046171 259 bp mRNA EST 25-JAN-2001 saa49e12.y1 Gm-c1060 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1060-215 5' similar to TR:Q43583 Q43583 HSR201 PROTEIN. ;,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Public Soybean EST Project
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/clone_lib="Gm-c1060"
                                                                                                                                                                                                                                                                                                                                                                                                      Length 258;
                                                                                                                                                                                                                                                                                                                10 others
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.2; DB 10;
Pred. No. 1.2e+03;
2; Mismatches 2;
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                                                                 /clone_lib="Lambda-PRL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Glycine max"
/strain="var columbia"
                         /db_xref="taxon:3702"
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                                            /clone="281H6T7"
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BG046171.1 GI:12494655
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76.5%;
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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Best Local Similarity
Matches 13; Conserv
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VERSION
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ORGANISM
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JOURNAL
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/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_rraf="taxon:3702"
/clone="168A5xp"
/clone="11b="Lambda-PRL2"
/
from root tissue of 2 week old seedlings for PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a KhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by KhoI digestion. The cDNA fragments were directionally cloned into the EcoRI. KhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."
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1 (bases 1 to 263)
Newman, T., deBrulin, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, E., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA651035 263 bp mRNA EST 05-JAN-1998
31149 Lambda-PRL2 Arabidopsis thaliana cDNA clone 168A5XP 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence entry for this EST has been reverse complimented and is being submitted in the sense orientation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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Pred. No. 1.2e+03;
2; Mismatches 2; Indels 0;
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MSU-DOE Plant Research Laboratory
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Fax: 517-353-9168
Email: 22313tcn@lbm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13_Universal.
Location/Qualifiers
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76.5%;
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DEFINITION RESULT 9 A1608251/c

ACCESSION VERSION KEYWORDS SOURCE

Matches

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ORIGIN

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Email: genome-resettc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci.p., Nishliyama.y., Westowcr,A., Itoh,M., Nagaoka,S., Sasaki,
N., Okazaki,Y., Huramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U. S. A. B. S. (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., A. Bibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                         Konno, H., Atzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Hara, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kayawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Taqawa, A., Takahashi, F., Tominaga, N., Toya, Y., Tan, K., Yano, K., Yano, M., Watahiki, A., Yokota, T., Yoshida, K., Yoshiki, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutherla; Rodentia; Sciurognathl; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
                           BB264508 294 bp mRNA EST 07-JUL-2000
BB264508 RIKEN full-length enriched, 10 days neonate cortex Mus
musculus CDNA clone A830015G22 3', mRNA sequence.
BB264508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/lab_host="DH108"
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
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                                                                                                                                          BB264508.1 GI:8960965
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                                                                                                                                                                                                       house mouse.
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                              LOCUS
DEFINITION
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JOURNAL
                                                                                                                    ACCESSION
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SOURCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 278)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
J. S., Sanler, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter
J. E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The Washu-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Seq primer: Primer name ambiguous
High quality sequence stop: 274.
Location/Qualifiers
1. 278
                                                                                                                                                                                                                                                                                                                                                                                                               pp mRNA EST 21-APR-1999
Solter mouse embryonic stem cell Mus musculus
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/db_xref="taxon:10090"
/clone="IMAGE:894569"
/clone="IMAGE:894569"
/dev_stage="embryo"
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                                                                               Length 263;
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Pred. No. 1.2e+03;
2; Mismatches 2;
                                                                                   Score 14.2; DB 10;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
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                                                                                   83.5%;
76.5%;
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76.5%;
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                          13; Conservative
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                                                                            Query Match
Best Local Similarity
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source

FEATURES

BASE COUNT ORIGIN

RESULT

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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. OBNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second /note-"Site_1: Sall; Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGGAGGACCAAGAGCTCTTTTTTTTTTTVN 3'], cDNA was /db_xref="taxon:10090" /clone="A330015G22" /clone_lib="RIKEN full-length enriched, 10 days neonate

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Editaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosladae; eurosida; Fabales; Fabaceae; Papilionoideae; Glycine. (bases 1 to 307)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,M., Sohurk,R., Watter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,Public Soybean EST Project
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW471629 307 bp mRNA EST 24-FEB-2000 sil3h01.yl Gm-c1029 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1029-1130 5' similar to TR:004201 004201 HYPERSENSITIVITY-RELATED GENE 201 ISOLOG.; , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: estewatson.wustl.edu

Email: estewatson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World

Parkway Circle St. Louis, Missouri 63134 For further information

call: (800) 430.0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)

427-3324 or contact: clones@genomesystems.com or

info@genomesystems.com web site: www.genomesystems.com

High quality sequence stop: 301.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1029-1130"
/clone=lib="Gm-c1029"
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                                                                                                                                                                                                                                         Length 294;
                                                                                                                                                                                                                                    Score 14.2; DB 129; Length
Pred. No. 1.2e+03;
Mismatches 2; Indels
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Public Soybean EST Project
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Fax: 314 286 1810
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.

1 (bases 1 to 324)

2 Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bohemaker, R., Marrah, Y., Hillier, L., Kucdab, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, Public Soybean EST Project

N. Unpublished (1999)

Other_ESTS: 8539412.x1

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

N. Deblic Soybean EST Project
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 386 1810
Fax: 314 57 3324 or Contact: clones@genomesystems.com or
Infogenomesystems.com web site: www.genomesystems.com
Seq primer: -40RP from Gibc.
High quality sequence stop: 311.
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                                                                                                                                                                                                                                                                                                       ö
site of the pSPORII vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
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Pred. No. 1.2e+03;
Mismatches 2; Indels 0;
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ilarity 76.5%;
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Contact: Mark Adams

Department of Enkiryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
    purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                           AQ034368 333 bp DNA GSS 11-JUL-1998
CIT-HSP-2319K4.TF CIT-HSP Homo sapiens genomic clone 2319K4, DNA
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Pred. No. 1.2e+03;
2; Mismatches 2; Indels 0;
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Pred. No. 1.2e+03;
2; Mismatches 2; 1
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/db_xref="taxon:9606"
/clone="2319K4"
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76.5%;
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Mammalia; Eutheria;
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Best Local Similarity 76.5
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., 181am, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb Jasmid inserts
Unpublished (2000)
were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding." 49 c 101 g 79 t 2 others
                                                                                                                                                                                                                                                                                                                                                              AZB13888 331 bp DNA GSS 20-FEB-2001
2M0081B21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0081B21 F, DNA sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                      Score 14.2; DB 102; Length 324;
Pred. No. 1.2e+03;
2; Mismatches 2; Indels 0;
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_cref="tuxoc2M0081B21"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0081 row: B column: 21
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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76.5%;
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Best Local Similarity 76.5
Matches 13; Conservative
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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KEYWORDS
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A2813888
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Gaps

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/note="Vector: pBluescriptSKmcUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp." 71 c 40 g 116 t
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                                                                                                                                                                                                                                                                Lycopersicon.
1 (bases 1 to 347)
Alcala.J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
                                                                                                                                                                 Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
3E460581 347 bp mRNA EST 27-JUL-2000 EST412000 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG31N6, mRNA sequence.
BE460581. GI:9504883
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                                                                                                                                                                                                                                                                                                                                                                                      ,S.D.
Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.5%; Score 14.2; DB 167; Length 347; 76.5%; Pred. No. 1.2e+03; 1ve 2; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 prime sequence.
Location/Qualifiers
1. 347
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cibG31N6"
/clone="cibG31N6"
/clone=lib="tomato breaker fruit, TIGR"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: David Frisch
Colmson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Email: dfrisch@CLEMSON.EDU
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91 GATTTTGGATGGGGAAA 75
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Best Local Similarity 76.5
Matches 13; Conservative
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                                                                                                                                                tomato.
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JOURNAL
COMMENT
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AUTHORS
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Search completed: November 5, 2001, 18:01:08 Job time: 14908 sec